

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 16:09:50 ; Search time 46 Seconds
(without alignments)
2180.765 Million cell updates/sec

Title: US-10-040-906A-2
Perfect score: 3314
Sequence: 1 MNVNLNNGRTICDAYNVVA.....GTQPELNMVFNLPPIY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 19Jun03.*

- 1: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1980.DAT.*
- 2: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1981.DAT.*
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- 4: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1983.DAT.*
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- 22: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
- 23: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
- 24: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3314	100.0	632	22	AAU02021
2	3048.5	92.0	633	15	AA356696
3	3046.5	91.9	635	22	AAU02043
4	3043.5	91.8	634	21	AA34259
5	3015.5	91.0	635	19	AAW75772
6	3010.5	90.8	633	21	AAW94260
7	3005.5	90.7	634	21	AAW94254
8	2974.5	89.8	633	13	AAW20030
9	2914.5	87.9	633	19	AAW75775

10	2913.5	87.9	633	19	AAW75774	Amino acid sequenc
11	2610.5	78.8	623	19	AAW75773	Amino acid sequenc
12	2582.5	77.9	625	22	AAU02044	B. thuringiensis t
13	1274.5	38.5	290	9	AA33002	Sequence of P-2 pr
14	1082	32.6	706	18	AAW31199	Bacillus popilliae
15	499	15.1	99	9	AA31356	Sequence of fragme
16	336.5	10.2	643	10	AA31462	67-kD protein toxi
17	336.5	10.2	643	17	AA31735	Bacillus thuringie
18	331.5	10.0	710	22	AAU02041	B. thuringiensis t
19	327.5	9.9	719	22	AA366908	Insecticidal prote
20	327.5	9.9	719	22	AA366910	Insecticidal prote
21	325.5	9.8	719	22	AA366911	Insecticidal prote
22	325	9.8	718	22	AA366907	Insecticidal prote
23	325	9.8	719	21	AA307073	Bacillus thuringie
24	324.5	9.8	719	11	AA308041	81 kD endotoxin de
25	324.5	9.8	719	22	AAU02095	Insecticidal prote
26	324.5	9.8	719	22	AA366909	Insecticidal prote
27	314.5	9.5	1217	22	AAU02092	Bacillus thuringie
28	311.5	9.4	1156	19	AAW46857	Bacillus thuringie
29	311.5	9.4	1156	20	AAW424960	B. thuringiensis t
30	311.5	9.4	1156	22	AAU02034	Amino acid sequenc
31	311	9.4	1157	20	AAW84587	Amino acid sequenc
32	311	9.4	1157	20	AAW84593	Amino acid sequenc
33	310.5	9.4	719	22	AA366912	Insecticidal prote
34	310	9.4	1157	20	AAW84580	Amino acid sequenc
35	309	9.3	1157	20	AAW84584	Amino acid sequenc
36	309	9.3	1157	20	AAW84590	Amino acid sequenc
37	309	9.3	1157	20	AAW84581	Amino acid sequenc
38	308	9.3	1157	20	AAW84583	Amino acid sequenc
39	308	9.3	1157	20	AAW84588	Amino acid sequenc
40	308	9.3	1157	20	AAW84589	Amino acid sequenc
41	308	9.3	1157	20	AAW84592	Amino acid sequenc
42	307	9.3	1138	15	AAW46225	Bacillus thuringie
43	307	9.3	1157	15	AAW48678	Insecticidal proto
44	307	9.3	1157	20	AAW84582	Amino acid sequenc
45	307	9.3	1157	20	AAW84586	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAU02021
ID AAU02021 standard; Protein; 632 AA.
XX
AC AAU02021;
XX
DT 29-AUG-2001 (first entry)
XX
DE B. thuringiensis toxic crystal protein, CryET31.
XX
DE Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
KW transgenic plant; corn, wheat; soybean; oat; cotton; rice; sorghum;
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
KW cotton leaf perforator; CryET31.
XX
OS Bacillus thuringiensis.
XX
FN WO200119859-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US25361.
XX
PR 15-SEP-1999; 99US-0153995.
PA (MONS) MONSANTO CO.
XX
PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
XX WPI; 2001-281518/29.
DR

DR N-PSDB; AAS02464.

XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides

PT and the polynucleotides that encode them, useful for increasing the

PT insect resistance of plant -

XX Claim 5; Page 102-103; 173pp; English.

XX The sequence represents a B. thuringiensis Lepidopteran-active

CC delta-endotoxin, crystal protein CryIIB. The lepidopteran-active B.

CC thuringiensis delta-endotoxin polypeptides may be used as compositions

CC that are applied to plant crops to protect them from insect damage. The

CC polynucleotides may be used in the production of transgenic plants that

CC express the insecticidal polypeptides and consequently have improved

CC insect resistance compared to non-transformed plants. Monocotyledonous or

CC dicotyledonous plants may be protected in this way, for example corn,

CC wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,

CC tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,

CC fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree

CC cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,

CC cotton leaf perforator and spruce budworm) may be affected by application

CC of the insecticidal polypeptides (full details given in specification).

XX SQ Sequence 632 AA;

Query Match 100.0%; Score 3314; DB 22; Length 632;

Best Local Similarity 100.0%; Pred. No. 3.7e-259;

Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEMWKRTHDSLYVAPIVGTVSSF 60

DB 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEMWKRTHDSLYVAPIVGTVSSF 60

QY 61 LLKKVSLIGKRIILSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLARVNAELEG 120

DB 61 LLKKVSLIGKRIILSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLARVNAELEG 120

QY 121 QANIREFNOQVDNLFNTQNPVLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180

DB 121 QANIREFNOQVDNLFNTQNPVLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180

QY 181 ANMHLSFIRDVVLNADENWISAAATLRTYQNLKNTTYSNYCINTYQAFRLNTRLHD 240

DB 181 ANMHLSFIRDVVLNADENWISAAATLRTYQNLKNTTYSNYCINTYQAFRLNTRLHD 240

QY 241 MLEFRTYMLNVEFVSVLSLFLKQSLVSSGANLYASGSGPQQTQSTQDWPFLYSLF 300

DB 241 MLEFRTYMLNVEFVSVLSLFLKQSLVSSGANLYASGSGPQQTQSTQDWPFLYSLF 300

QY 301 QVNSNYVLNFGSGARLTQTFNIGLPGTTTTHALLAARVNYSGVSGDYGAVFNQNF 360

DB 301 QVNSNYVLNFGSGARLTQTFNIGLPGTTTTHALLAARVNYSGVSGDYGAVFNQNF 360

QY 361 CSTFLPPLLTTPFVRSWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPDY 420

DB 361 CSTFLPPLLTTPFVRSWLDGSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYFPDY 420

QY 421 FIRNISGVLVVRNEDLRPLHYNEIRNIESPSGTGGLRAYMVSVNRKNNIYAVHENG 480

DB 421 FIRNISGVLVVRNEDLRPLHYNEIRNIESPSGTGGLRAYMVSVNRKNNIYAVHENG 480

QY 481 TMIHLAPEDYTGFTIISPIHATQVNNQTRTFISEKFGNQDLSLRPEQNTTARYTLRNGN 540

DB 481 TMIHLAPEDYTGFTIISPIHATQVNNQTRTFISEKFGNQDLSLRPEQNTTARYTLRNGN 540

QY 541 SYNLVLRVSSLCNSTIRVTINGRVTYASNVNTTNDGVNDNGARFLDINNNGVVASDNT 600

DB 541 SYNLVLRVSSLCNSTIRVTINGRVTYASNVNTTNDGVNDNGARFLDINNNGVVASDNT 600

QY 601 NVPLDINVNTNSGTQFELMNMIFVPTNLPIY 632

DB 601 NVPLDINVNTNSGTQFELMNMIFVPTNLPIY 632

RESULT 2

AAAR56696

XX AAR56696 standard; Protein; 633 AA.

XX AC AAR56696;

XX DT 25-MAR-2003 (updated)

XX DT 27-MAR-1995 (first entry)

XX DE CryIIA insecticidal crystal protein.

XX CryIIA; CryIIIA; CryIIB; CryC; P-2; CryBI; insecticidal protein crystal;

XX lepidoptera; environmental insecticide; Bacillus thuringiensis; toxic;

XX probe; hybridisation.

XX OS Bacillus thuringiensis.

XX US5338544-A.

XX PD 16-AUG-1994.

XX PF 26-FEB-1993; 93US-0023736.

XX PR 16-APR-1987; 87US-0039542.

XX PR 11-JUL-1989; 89US-0379015.

XX PR 28-AUG-1991; 91US-0751452.

XX PR 26-FEB-1993; 93US-0023736.

XX PA (ECOG-) ECOGEN INC.

XX PI Donovan WP;

XX WPI; 1994-263236/32.

XX N-PSDB; AAQ71025.

XX New Cry IIB protein - obtd. from the cry II B gene in Bacillus

XX thuringiensis var. Kurstaki, active against lepidopteran insects

XX Example 2; Fig 2A-2C; 39pp; English.

XX This sequence shows the amino acid sequence of CryIIA protein.

XX The CryIIA gene was used as a probe to identify CryIIA related

XX sequences, ie. CryIIB. CryIIB encodes an insecticidal crystal

XX protein isolated from Bacillus thuringiensis var. kurstaki. It

XX produces crystal proteins during sporulation which are specifically

XX toxic to certain orders and species of insects, esp. Lepidoptera.

XX CryIIB can be used in compositions used as environmentally acceptable

XX insecticides. (See also AAR56697-8)

XX (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 633 AA;

Query Match 92.0%; Score 3048.5; DB 15; Length 633;

Best Local Similarity 90.7%; Pred. No. 1.1e-237;

Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

QY 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEMWKRTHDSLYVAPIVGTVSSF 60

DB 1 MNNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEMWKRTHDSLYVAPIVGTVSSF 60

QY 61 LLKKVSLIGKRIILSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLARVNAELEG 120

DB 61 LLKKVSLIGKRIILSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLARVNAELEG 120

QY 121 QANIREFNOQVDNLFNTQNPVLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180

DB 121 QANIREFNOQVDNLFNTQNPVLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180

QY 181 ANMHLSFIRDVVLNADENWISAAATLRTYQNLKNTTYSNYCINTYQAFRLNTRLHD 240

DB 181 ANMHLSFIRDVVLNADENWISAAATLRTYQNLKNTTYSNYCINTYQAFRLNTRLHD 240

QY 241 MLEBRTYMLNVEYVWSLWKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
 Db 241 MLEBRTYMLNVEYVWSLWKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300
 QY 301 QVNSNYLVNGFSGARLTQTPNIGGLPGTTHALLAARVNYSGVSSGDIGAV-FNQNF 359
 Db 301 QVNSNYLVNGFSGARLTQTPNIGGLPGTTHALLAARVNYSGVSSGDIGAV-FNQNF 359
 QY 360 SCSTFLPLLTTPVRSWLDGSGRGVNTVNMWQTESFESTGLRCGAFARGNSNYFPD 419
 Db 361 NCSTVLPPLSTPVRWSLDSGTDEGVATSTNMWQTESFESTGLRCGAFARGNSNYFPD 420
 QY 420 YFIRNIGSVPLVVRNEDLRPLHNEIRNIESPSGTGGLRAYVSVHNRKNYIAVHN 479
 Db 421 YFIRNIGSVPLVVRNEDLRPLHNEIRNIESPSGTGGLRAYVSVHNRKNYIAVHN 480
 QY 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNGDGLRFEQSNNTTARYTLRG 539
 Db 481 GTMIHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNGDGLRFEQSNNTTARYTLRG 540
 QY 540 NSYNLYLRVSSLGNSSTIRVTINGRVYASVNTTNNNDGVNDNGAREFIDINMGVVASDN 599
 Db 541 NSYNLYLRVSSLGNSSTIRVTINGRVYASVNTTNNNDGVNDNGAREFIDINMGVVASDN 600
 QY 600 TNYPLDINVTNSGTQFELMNMFPVPTNLPPIY 632
 Db 601 TNYPLDINVTNSGTQFELMNMFPVPTNLPPIY 633

RESULT 3

AAU02043

ID AAU02043 standard; Protein; 635 AA.

XX

AC AAU02043;

XX

DT 29-AUG-2001 (first entry)

XX

DE B. thuringiensis toxic crystal protein, CryET72.

XX

KW Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
 transgenic plant; corn; wheat; soybean; oat; cotton; rice; sorghum;
 sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
 pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
 cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
 cotton leaf perforator; CryET72.

XX

OS Bacillus thuringiensis.

XX

PN W0200119859-A2.

XX

PD 22-MAR-2001.

XX

PF 13-SEP-2000; 2000WO-US25361.

XX

PX 15-SEP-1999; 99US-0153995.

XX

PR (MONS) MONSANTO CO.

XX

PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;

XX

DR WPI; 2001-281518/29.

XX

DR N-PSDB; AAS02486.

XX

Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
 and the polynucleotides that encode them, useful for increasing the
 insect resistance of plant -

XX

PS Claim 5; Page 158-160; 173pp; English.

XX

CC The sequence represents a B. thuringiensis Lepidopteran-active
 delta-endotoxin, crystal protein CryET72. The Lepidopteran-active B.
 thuringiensis delta-endotoxin polypeptides may be used as compositions
 that are applied to plant crops to protect them from insect damage. The

CC

CC polynucleotides may be used in the production of transgenic plants that
 express the insecticidal polypeptides and consequently have improved
 insect resistance compared to non-transformed plants. Monocotyledonous or
 dicotyledonous plants may be protected in this way, for example corn,
 wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
 tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 cotton leaf perforator and spruce budworm) may be affected by application
 of the insecticidal polypeptides (full details given in specification).

XX

SQ Sequence 635 AA;

XX

Query Match 91.9%; Score 3046.5; DB 22; Length 635;

Best Local Similarity 90.9%; Pred. No. 1.6e-237;

Matches 577; Conservative 31; Mismatches 24; Indels 3; Gaps 2;

QY 1 MNVNVANGRTTICADYNNVAHDPSFEHKSLDTRIRKEMWETKTHSLYVAPVGVTSF 60

Db 1 MNVNVANGRTTICADYNNVAHDPSFEHKSLDTRIRKEMWETKTHSLYVAPVGVTSF 60

QY 61 LKKVGLSLGKRLISELWGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARNVAEGL 120

Db 61 LKKVGLSLGKRLISELWGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARNVAEGL 120

QY 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTWQQLFLNRLPQFQIQGYQLLLPLPAQA 180

Db 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTWQQLFLNRLPQFQIQGYQLLLPLPAQA 180

QY 181 ANMHLFIRDVLNADWEGISATLRYQNYLKNYTEVSNYCINTYQTAPRGLNRLHD 240

Db 181 ANMHLFIRDVLNADWEGISATLRYQNYLKNYTEVSNYCINTYQTAPRGLNRLHD 240

QY 241 MLEFRTYMLNVEYVWSLWKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300

Db 241 MLEFRTYMLNVEYVWSLWKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLYSLF 300

QY 301 QVNSNYLVNGFSGARLTQTPNIGGLPGTTHALLAARVNYSGVSSGDIGAV-FNQNF 359

Db 301 QVNSNYLVNGFSGARLTQTPNIGGLPGTTHALLAARVNYSGVSSGDIGAV-FNQNF 359

QY 360 SCSTFLPLLTTPVRSWLDGSGRGVNTVNMWQTESFESTGLRCGA--FTARGNSNYF 417

Db 361 NCSTVLPPLSTPVRWSLDSGTDEGVATSTNMWQTESFESTGLRCGAFPSARGNSNYF 420

QY 418 PDYFIRNIGSVPLVVRNEDLRPLHNEIRNIESPSGTGGLRAYVSVHNRKNYIAVH 477

Db 421 PDYFIRNIGSVPLVVRNEDLRPLHNEIRNIESPSGTGGLRAYVSVHNRKNYIAVH 480

QY 478 ENGTMHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNGDGLRFEQSNNTTARYTLRG 537

Db 481 ENGTMHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNGDGLRFEQSNNTTARYTLRG 540

QY 538 NGNSYNLYLRVSSLGNSSTIRVTINGRVYASVNTTNNNDGVNDNGAREFIDINMGVVAS 597

Db 541 NGNSYNLYLRVSSLGNSSTIRVTINGRVYASVNTTNNNDGVNDNGAREFIDINMGVVAS 600

QY 598 DNTNVPLDINVTNSGTQFELMNMFPVPTNLPPIY 632

Db 601 DNTNVPLDINVTNSGTQFELMNMFPVPTNLPPIY 635

RESULT 4

AAV94259

ID AAV94259 standard; Protein; 634 AA.

XX

AC AAV94259;

XX

DT 28-JUL-2000 (first entry)

XX

DE Cry2Aa delta-endotoxin.

XX

KW Transgenic plant; insect resistance; cry2Aa delta-endotoxin; Coleopteran;

Query Match 91.0%; Score 3015.5; DB 19; Length 635;
Best Local Similarity 90.2%; Pred. No. 5.2e-235;
Matches 573; Conservative 30; Mismatches 29; Indels 3;

QY 1 MNVNLNGRTTICDAYNVVAHDPSPFEHKSLEDTIRKEWMEKRTDHSLSYVAPIVGTVSSF 60
Db 1 MNVNLNGRTTICDAYNVVAHDPSPFEHKSLEDTIRKEWMEKRTDHSLSYVAPIVGTVSSF 60
QY 61 LKKGVSIGKRIISLSELMGLIFPSSGNTLMQDILRETEQFLNORLNTDTLARVNAEGL 120
Db 61 LKKGVSIGKRIISLSELMGLIFPSSGNTLMQDILRETEQFLNORLNTDTLARVNAEGL 120
QY 121 QANIREFNOQVDNLFNPTQNPVLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANIREFNOQVDNLFNPTQNPVLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
QY 181 ANHLSPFIRVDVLNADEWIGISAATLRTYQNLKNTYEVSNYNTQTAFGLNTRLHD 240
Db 181 ANHLSPFIRVDVLNADEWIGISAATLRTYQNLKNTYEVSNYNTQTAFGLNTRLHD 240
QY 241 MLEFRTYMLNVPFVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSDMPFLYSLF 300
Db 241 MLEFRTYMLNVPFVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSDMPFLYSLF 300
QY 301 QVNSNYLVNGFSGARLTQTFPNIGLPGTTTTTHALLAARVNSYSGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYLVNGFSGARLTQTFPNIGLPGTTTTTHALLAARVNSYSGVSSGDIGAV-FNQNF 359
QY 360 SCSTFLPPLLTTPFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGA--FTARGNSYF 417
Db 360 SCSTFLPPLLTTPFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGA--FTARGNSYF 417
QY 361 NCSTFLPPLLTTPFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGA--FTARGNSYF 420
Db 361 NCSTFLPPLLTTPFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGA--FTARGNSYF 420
QY 418 PDYFIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIYAVH 477
Db 421 PDYFIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIYAAH 480
QY 478 ENGTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKEGNOGDSLRFEQSNNTARYTLRG 537
Db 481 ENGTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKEGNOGDSLRFEQSNNTARYTLRG 540
QY 538 NGNSNYLVRSVSSLGNSITRTVINGRVYTAASNVTNTNNDGVNDNGARFLDINMGNVVAS 597
Db 541 NGNSNYLVRSVSSLGNSITRTVINGRVYTAASNVTNTNNDGVNDNGARFSDINMGNVVAS 600
QY 598 DNTNVPDLINTFNSGTOFELMNMIFVPTNLPPIY 632
Db 601 DNTNVPDLINTFNSGTOFELMNMIFVPTNLPPIY 635

RESULT 6
AA94260
ID AA94260 standard; Protein; 633 AA.
AC AA94260;
XX
DT 28-JUL-2000 (first entry)
TX
DE Cry2Ab delta-endotoxin.
XX
KW Transgenic plant; insect resistance; cry2Ab delta-endotoxin; Coleopteran;
KW Lepidopteran; Dipteran; plastid transit peptide; PTP; insecticidal;
KW plastid targeting peptide.
XX
OS Bacillus thuringiensis.
XX
PN WO200026371-A1.
XX
PD 11-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US26086.
XX
PR 04-NOV-1998; 98US-0186002.
XX
PA (MONS) MONSANTO CO.
XX
PI Corbin DR, Romano CP;
XX

WPI; 2000-376130/32.
N-PSDB; AAA15566.
New method of expressing insecticidal proteins in plants transformed with a Bacillus thuringiensis delta-endotoxin encoding gene resulting in effective control of susceptible target pests -
Claim 14; Page 100-101; 104pp; English.
The present sequence is the Cry2Ab delta-endotoxin. Delta-endotoxins are produced by Bacillus thuringiensis during sporulation. These proteins are toxic to certain species of insect e.g. Lepidopteran and Coleopteran larvae. An insect-resistant transgenic plant has been constructed which contains the cry2Ab gene. The cry2Ab gene would be transferred into plants via expression vectors, which subsequently allow high expression of the cry2Ab gene. The present sequence lacks Dipteran inhibitory activity. Protection may be attained against insects such as Ostrinia spp., Diatraea spp., Heliothis spp., and Spodoptera spp., in Zea mays; Heliothis virescens, Heliothis spp., Pectinophora spp., in Gossypium hirsutum; Anticarsia spp., Pseudoplusia spp., Epinotia spp., in Glycine max; and Scirpophaga incertulas in Oryza sativa. Expression of the cry2Ab gene by a plant cell produces a fusion protein comprising an amino-terminal plastid transit peptide (PTP) covalently linked to the delta-endotoxin. The fusion protein functions to localise the delta-endotoxin to a subcellular organelle or compartment.
Sequence 633 AA;
Query Match 90.88; Score 3010.5; DB 21; Length 633;
Best Local Similarity 89.74; Pred. No. 1.3e-234;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;
QY 1 MNVNLNGRTTICDAYNVVAHDPSPFEHKSLEDTIRKEWMEKRTDHSLSYVAPIVGTVSSF 60
Db 1 MNSVLSNGRTTICDAYNVVAHDPSPFEHKSLEDTIRKEWMEKRTDHSLSYVAPIVGTVSSF 60
QY 61 LKKGVSIGKRIISLSELMGLIFPSSGNTLMQDILRETEQFLNORLNTDTLARVNAEGL 120
Db 61 LKKGVSIGKRIISLSELMGLIFPSSGNTLMQDILRETEQFLNORLNTDTLARVNAEGL 120
QY 121 QANIREFNOQVDNLFNPTQNPVLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANIREFNOQVDNLFNPTQNPVLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
QY 181 ANHLSPFIRVDVLNADEWIGISAATLRTYQNLKNTYEVSNYNTQTAFGLNTRLHD 240
Db 181 ANHLSPFIRVDVLNADEWIGISAATLRTYQNLKNTYEVSNYNTQTAFGLNTRLHD 240
QY 241 MLEFRTYMLNVPFVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSDMPFLYSLF 300
Db 241 MLEFRTYMLNVPFVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSDMPFLYSLF 300
QY 301 QVNSNYLVNGFSGARLTQTFPNIGLPGTTTTTHALLAARVNSYSGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYLVNGFSGARLTQTFPNIGLPGTTTTTHALLAARVNSYSGVSSGDIGAV-FNQNF 359
QY 360 SCSTFLPPLLTTPFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGAFTARGNSYFPD 419
Db 361 NCSTFLPPLLTTPFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGAFTARGNSYFPD 420
QY 420 YFIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIYAVH 479
Db 421 YFIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIYAVH 480
QY 480 GTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKEGNOGDSLRFEQSNNTARYTLRG 539
Db 481 GTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKEGNOGDSLRFEQSNNTARYTLRG 540
QY 540 NSYNLYLVRSVSSLGNSITRTVINGRVYTAASNVTNTNNDGVNDNGARFLDINMGNVVASDN 599
Db 541 NSYNLYLVRSVSSLGNSITRTVINGRVYTAASNVTNTNNDGVNDNGARFSDINMGNVVASDN 600
QY 600 TNPVLDINTFNSGTOFELMNMIFVPTNLPPIY 632

```

Db      601 SDVPLDINVTLNSGTQFDLMNMLVPTNISPLY 633
      :::::::::::::::::::::::::::::::::::::::::::::
RESULT 7
AA94254
ID AA94254 standard; Protein; 634 AA.
XX
AC AA94254;
XX
DT 28-JUL-2000 (first entry)
XX
DE DE
XX
KW Transgenic plant; insect resistance; cry2Ab delta-endotoxin; Coleopteran;
KW Lepidopteran; Dipteran; plastid transit peptide; PTP; insecticidal;
KW plastid targeting peptide.
XX
OS Bacillus thuringiensis.
XX
FN WO200026371-A1.
XX
PD 11-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US26086.
XX
PR 04-NOV-1998; 98US-0186002.
XX
PA (MONS ) MONSANTO CO.
XX
PI Corbin DR, Romano CP;
XX
DR WPI; 2000-376130/32.
XX
N-PSDB; AAA15556.
XX
New method of expressing insecticidal proteins in plants transformed
PT with a Bacillus thuringiensis delta-endotoxin encoding gene resulting
PT in effective control of susceptible target pests -
XX
PS Claim 14; Page 82-83; 104pp; English.
XX
The present sequence is the Cry2Ab delta-endotoxin. Delta-endotoxins are
CC produced by Bacillus thuringiensis during sporulation. These proteins are
CC toxic to certain species of insect e.g. Lepidopteran and Coleopteran
CC larvae. An insect-resistant transgenic plant has been constructed which
CC contains the cry2Ab gene. The cry2Ab gene would be transferred into
CC plants via expression vectors, which subsequently allow high expression
CC of the cry2Ab gene. The present sequence lacks Dipteran inhibitory
CC activity. Protection may be attained against insects such as Ostrina
CC spp., Diatraea spp., Helicoverpa spp., and Spodoptera spp., in Zea mays;
CC Heliothis virescens, Helicoverpa spp., Pectinophora spp., in Gossypium
CC hirsutum; Anticarsia spp., Pseudoplusia spp., Epinotia spp., in Glycine
CC max; and Scirpophaga incertulas in Oryza sativa. Expression of the
CC cry2Ab gene by a plant cell produces a fusion protein comprising
CC an amino-terminal plastid transit peptide (PTP) covalently linked to the
CC delta-endotoxin. The fusion protein functions to localise the
CC delta-endotoxin to a subcellular organelle or compartment.
XX
SQ Sequence 634 AA;
Query Match 90.7%; Score 3005.5; DB 21; Length 634;
Best Local Similarity 89.7%; Pred. No. 3.3e-234;
Matches 567; Conservative 39; Mismatches 25; Indels 1; Gaps 1;
QY 2 NNVLNNGRTTICDAYNVVAHDPFSEHKSLDTIRKEMMEWRKTDHSLYVPIVGTVSFL 61
Db 3 NSVLNSGRTTICDAYNVAAHDPFSEHKSLDTVQKTEWKNNHSLYLDPIVGTVASFL 62
QY 62 LKKVCSLTKRILSELWGLIPFSGSTNLMQDILRETEFLQRLNTDILARVNAELGLQ 121
Db 63 LKKVCSLTKRILSELRLNLIIPFSGSTNLMQDILRETEFLQRLNTDILARVNAELGLQ 122
QY 122 ANIREFNQVDNVLNPTNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 181
      :::::::::::::::::::::::::::::::::::::::::::::::
Db      123 ANVEEFNRQVDNVLNPNRNVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 182
QY      182 NMHLSPTRDVLNDAEWGISAAATLRTYQNLKNTTYSNYCINTYQAFRGLNTRLHDM 241
Db      183 NLHLSPTRDVLNDAEWGISAAATLRTYQNLKNTTYSNYCINTYQAFRGLNTRLHDM 242
QY      242 LEFRYTMFLNVFEYVSIWSLTKYOSLAVSSGANLYASGSGPQOQTSQDWPFLYSIFQ 301
Db      243 LEFRYTMFLNVFEYVSIWSLTKYOSLAVSSGANLYASGSGPQOQTSQDWPFLYSIFQ 302
QY      302 VNSNYVLNFGSGARLTQTFFNIGLPGCTTTTHALLAARVNSGVSVDGICA-VFNQNF 360
Db      303 VNSNYVLNFGSGARLNTFFNIVGLPGSTTTTHALLAARVNSGVSVDGICASFQNF 362
QY      361 CSTFLPPLLPFFVRSWLDSDGSGVNTVNTWQTESPESTLGLRCGAFARGNSNYPPDY 420
Db      363 CSTFLPPLLPFFVRSWLDSDGSGREGVATVNTWQTESPESTLGLRCGAFARGNSNYPPDY 422
QY      421 FIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIYAVHENG 480
Db      423 FIRNISGVPLVVRNEDLRRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNIYAVHENG 482
QY      481 TMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGQSDSLRPEQNTTARYTLRNGN 540
Db      483 SMHLAPNDYTGFTTISPIHATQVNNQTRTFISEKFGQSDSLRPEQNTTARYTLRNGN 542
QY      541 SYNLYLRVSSLGNSITRTVINGRVYTASNVTNTNDGVNDNGARFLDINMGNVVADNT 600
Db      543 SYNLYLRVSSLGNSITRTVINGRVYTASNVTNTNDGVNDNGARFLDINMGNVVADNT 602
QY      601 NVPLDINVNTNSGTQFELMNMIFVPTNLPPY 632
Db      603 DVPLDINVNTNSGTQFELMNMILVPTNISPLY 634
      :::::::::::::::::::::::::::::::::::::::::::::::
RESULT 8
AAR20030
ID AAR20030 standard; Protein; 633 AA.
XX
AC AAR20030;
XX
DT 07-APR-1992 (first entry)
XX
DE Bacillus thuringiensis CryIIB crystal toxin.
XX
KW B.t. crystal protein; insecticide; Lepidoptera; larva; corn earworm;
KW Heliothis zea.
XX
OS Bacillus thuringiensis.
XX
FN US5073632-A.
XX
PD 17-DEC-1991.
XX
PE 11-JUL-1989; 89US-0379015.
XX
PR 11-JUL-1989; 89US-0379015.
XX
PR 16-APR-1987; 87US-0039542.
XX
PA (ECOG-) ECOGEN INC.
XX
PI Donovan WP;
XX
DR WPI; 1992-016224/02.
XX
N-PSDB; AAQ20202.
XX
PT Bacillus thuringiensis cryIIB protein gene - used to obtain the
PT protein for use as an insecticidal cpd. against lepidopteran
XX insects
XX
PS Disclosure; Fig 6; 30pp; English.
XX

```

CC The cryIIb gene was isolated from a B.t. strain using the cryIIa
 CC gene as probe. The cryIIb gene encodes a 633 amino acid protein of
 CC calculated mol. wt. 70.749. The insecticidal toxin CryIIb is twice
 CC as toxic as the CryIIa protein against the lepidopteran Heliothis
 CC zea.
 XX
 SQ Sequence 633 AA;

Query Match 89.8%; Score 2974.5; DB 13; Length 633;
 Best Local Similarity 88.8%; Pred. No. 1.1e-231;
 Matches 562; Conservative 39; Mismatches 31; Indels 1; Gaps 1;

Qy 1 MNVNLNGRTTICDAYNVVAHDPPSPFHKSLDTIRKEMWKRTHDSLYVAPIVGTVSSP 60
 Db 1 MNSVLNNGRTTICDAYNVVAHDPPSPFHKSLDTIRKEMWKRTHDSLYVAPIVGTVSSP 60

Qy 61 LLKKVGLIGKRISELWGLIFPSSGNTLMQDILRETEQFLNQLNRTDTLARVNAELGL 120
 Db 61 LLKKVGLIGKRISELWGLIFPSSGNTLMQDILRETEQFLNQLNRTDTLARVNAELGL 120

Qy 121 QANREFNQVDNPLNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
 Db 121 QANVEEFNRQVDNPLNPNRNVPLSITSSVNTMQQLFLNRLPQFQMGYQLLLPLFAQA 180

Qy 181 ANMHLSPTRDVVLNADWEGISAATLRTYQNYLKNYTTESYNYCINTYTAPRGLNRLHD 240
 Db 181 ANLHLSFTRDVLNADWEGISAATLRTYQNYLKNYTTESYNYCINTYTAPRGLNRLHD 240

Qy 241 MLEPRTYMLNVEFVYSWLSFKYQSLVSSGANLYASGSGPQQTQSTQDWPFLYSLF 300
 Db 241 MLEPRTYMLNVEFVYSWLSFKYQSLVSSGANLYASGSGPQQTQSTQDWPFLYSLF 300

Qy 301 QVNSNYVLNGFSGARLTOTFPNIGLPGTTTTALLAARVNSGVSDDIGA-VFNQNF 359
 Db 301 QVNSNYVLNFAFSRRLSNTFENIVALPGSTTTALLAATVNSGVSDDIGA-SFFNQNF 360

Qy 360 SCSTFLPPLLTTPFVRSWLDSDGDRGVNTVNTWQTESFESTLGLRCGAFTARGNSNYP 419
 Db 361 NCSTFLPPLLTTPFVRSWLDSDGDRGVNTVNTWQTESFESTLGLRCGAFTARGNSNYP 420

Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYAVHEN 479
 Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYAVHEN 480

Qy 480 GTMIHLAPEDYTGFTISPIHATQVNNOTRTFISEKFGQDGLRFEQNTTARYTLRGNG 539
 Db 481 GSMIHLAPNDYTAFTISPIHATQVNNOTRTFISEKFGQDGLRFEQNTTARYTLRGNG 540

Qy 540 NSYNLYLRVSSLSGNTSTIRVTNGRVYTTASNVNTTNDGVDNDNGARFLDINMGNVVASDN 599
 Db 541 NSYNLYLRVSSLSGNTSTIRVTNGRVYTTATNVNTTNDGVDNDNGARFSDINIGNVVASSN 600

Qy 600 TNVPLDINVTNSGTFQFELMIMFVPTNLPYI 632
 Db 601 SDVPLDINVTLSGTFQFELMIMLVPTNLSPLY 633

RESULT 9
 AA75775
 ID AA75775 standard; Protein; 633 AA.
 XX
 AC AA75775;
 XX
 DT 02-DEC-1998 (first entry)
 XX
 DE Amino acid sequence of lepidoteran-active 8612 toxin.
 XX
 KW 8612 toxin; PCR; primer; amplification; Bacillus thuringiensis; probe;
 KW lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;
 KW Helicoverpa zea; hybridisation.
 XX
 OS Bacillus thuringiensis.
 XX

PN W09840490-A1.
 XX 17-SEP-1998.
 XX 13-MAR-1998; 98WO-US05081.
 XX 13-MAR-1997; 97US-0040512.
 XX (MYCO) MYCOGEN CORP.
 XX Muller-Cohn J, Narva KE, Schnepf HE;
 DR WPI; 1998-506734/43.
 DR N-PSDB; AAV52612.
 XX New insecticidal Bacillus thuringiensis toxins - useful for
 PT controlling lepidopteran pests, especially Ostrinia nubilalis,
 PT Heliothis virescens and Helicoverpa zea
 XX Claim 5; Pages 36-38; 50pp; English.
 XX This is the amino acid sequence of a novel Bacillus thuringiensis toxin
 CC used in the method of the invention, to control lepidopteran pests.
 CC The new toxins are useful as pesticides, especially for the control of
 CC Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The
 CC polynucleotide coding sequences are useful for recombinant expression
 CC of the toxins and the primers, together with probes derived from the
 CC new sequences, are useful for the identification and characterisation
 CC of novel genes that encode pesticidal toxins.
 XX
 SQ Sequence 633 AA;

Query Match 87.9%; Score 2914.5; DB 19; Length 633;
 Best Local Similarity 87.0%; Pred. No. 7.6e-227;
 Matches 551; Conservative 44; Mismatches 37; Indels 1; Gaps 1;

Qy 1 MNVNLNGRTTICDAYNVVAHDPPSPFHKSLDTIRKEMWKRTHDSLYVAPIVGTVSSP 60
 Db 1 MNVNLNGRTTICDAYNVVAHDPPSPFHKSLDTIRKEMWKRTHDSLYVAPIVGTVSSP 60

Qy 61 LLKKVGLIGKRISELWGLIFPSSGNTLMQDILRETEQFLNQLNRTDTLARVNAELGL 120
 Db 61 LLKKVGLIGKRISELWGLIFPSSGNTLMQDILRETEQFLNQLNRTDTLARVNAELGL 120

Qy 121 QANREFNQVDNPLNPTQNPVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQA 180
 Db 121 QANVEEFNRQVDNPLNPNRNVPLSITSSVNTMQQLFLNRLPQFQMGYQLLLPLFAQA 180

Qy 181 ANMHLSPTRDVVLNADWEGISAATLRTYQNYLKNYTTESYNYCINTYTAPRGLNRLHD 240
 Db 181 ANIHLSPTRDVVLNADWEGISAATLRTYQNYLKNYTTESYNYCINTYTAPRGLNRLHD 240

Qy 241 MLEPRTYMLNVEFVYSWLSFKYQSLVSSGANLYASGSGPQQTQSTQDWPFLYSLF 300
 Db 241 MLEPRTYMLNVEFVYSWLSFKYQSLVSSGANLYASGSGPQQTQSTQDWPFLYSLF 300

Qy 301 QVNSNYVLNGFSGARLTOTFPNIGLPGTTTTALLAARVNSGVSDDI-GAVFNQNF 359
 Db 301 QVNSNYVLNGFSGARLTOTFPNIGLPGTTTTALLAARVNSGVSDDI-GAVFNQNF 360

Qy 360 SCSTFLPPLLTTPFVRSWLDSDGDRGVNTVNTWQTESFESTLGLRCGAFTARGNSNYP 419
 Db 361 NCNTISPLSTSFVRSWLDSDGDRGVNTVNTWQTESFESTLGLRCGAFTARGNSNYP 420

Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYAVHEN 479
 Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNYAVHEN 480

Qy 480 GTMIHLAPEDYTGFTISPIHATQVNNOTRTFISEKFGQDGLRFEQNTTARYTLRGNG 539
 Db 481 GTMIHLAPEDYTGFTISPIHATQVNNOTRTFISEKFGQDGLRFEQNTTARYTLRGNG 540

Qy 540 NSYNLYLRVSSLSGNTSTIRVTNGRVYTTASNVNTTNDGVDNDNGARFLDINMGNVVASDN 599

CC polynucleotide coding sequences are useful for recombinant expression
 CC of the toxins and the primers, together with probes derived from the
 CC new sequences, are useful for the identification and characterisation
 CC of novel genes that encode pesticidal toxins.

XX SQ Sequence 623 AA;

Query Match 78.8%; Score 2610.5; DB 19; Length 623;

Best Local Similarity 80.3%; Pred. No. 2.9e-202;

Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

Qy 1 MNNVNNGRITTCIDAYNVVAHDPFSEHKSLDTIRKEWMEKRTDHSLYVAPIVGTVSSP 60
 Db 1 MNNVNSGRNTTCHANNVVAHDPFSEHKSLNTIEKEWKEKRTDHSLYVAPIVGTVGSF 60
 Qy 61 LLKKVGLIGKRILSELWGLIPFSGSTNLMODILRETEQFLNQRLNTDTLARVNAELEG 120
 Db 61 LLKKVGLSVGRILSELQNLIPFSGSIDLMQELIRATEQFINQLNADTLGRVNAELAGL 120
 Qy 121 QANIRENQVDNPLNPTQNPVPLSITSSVNTMQOLFNLRLPQFVQGYQLLLPLPAQA 180
 Db 121 QANVAEFNRQVDNPLNPNQNPVPLAIDSNTLQQLFLSLRPLQFQIQGYQLLLPLPAQA 180
 Qy 181 ANMHLSPFRDVLNADWEGISAATLRTYQNYLKNVTTYEYSNYCINTYQTAFRLNTRLHD 240
 Db 181 ANLHLSFIRDVLNADWEGISAATVTRYDRHLNFTRDYSNYCINTYQTAFRLNTRLHD 240
 Qy 241 MLEFRTYMLNVEFYVSIWLSFKYQSLVSSGANLYASGSGP--TQSFTHNWFYLSLF 300
 Db 241 MLEFRTYMLNVEFYVSIWLSFKYQSLVSSGANLYASGSGP--TQSFTHNWFYLSLF 298
 Qy 301 QVNSNYLVNGFSGARLTQTFPNIGGLPGTTTHALLAARVNSYSGVSSGDIG-AVFNQNF 359
 Db 299 QVNSNYLVNGLSGARTTITFPNIGGLPGSTTTQTLHFARINRYRGVSSSRIGQANLNQNF 358
 Qy 360 SCSTFLPPLTPFVRSWLDSDRGVNTVNTWOTESFESTLGRCCGAFARGNSYFPD 419
 Db 359 NISTLFPNLPQTFPIRSWLDSDRGVNTVNTWOGSAFETTL-LRFSIFSARGNSYFPD 417
 Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSTGPGGLRAYMVSVHNRKNNIYAVHEN 479
 Db 418 YFIRNISGVVGTISNADLARLPHENEIRDI---GTTA--VASLTVVHNRKNNIYDTHEN 471
 Qy 480 GTMIHLAPEDYGTGISPIHATQVNNQTRTFISEKFGNQGSLRPFESNTTARYTLRGNG 539
 Db 472 GTMIHLAPNDYGTFTSPFIHATQVNNQTRTFISEKYGNGQSLRFLSNTTARYTLRGNG 531
 Qy 540 NSYNLYRVSLGNTIRVTINGRVYTAASNVTNTTNDGVDNGARFLDINMGVNVASDN 599
 Db 532 NSYNLYRVSSIGSTIRVTINGRVYTA-NVNTTNTNDGVDLNDGAREFSDINIGNVVASN 590
 Qy 600 TNVPLDINVTNFGTQFELNMIVPTNLPPIY 632
 Db 591 TNVPLDIOVTENGPNQFELNMIVPTNPSPLY 623

RESULT 12

AAU02044

ID AAU02044 standard; Protein; 625 AA.

XX AC AAU02044;

XX DT 29-AUG-2001 (first entry)

XX DE B. thuringiensis toxic crystal protein, CryET73.

XX KW Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
 XX KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; yam; sorghum;
 XX KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
 XX KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
 XX KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
 XX KW cotton leaf perforator; CryET73.

OS Bacillus thuringiensis.

XX PN WO200119859-A2.

XX PD 22-MAR-2001.

XX PF 13-SEP-2000; 2000WO-US25361.

XX PR 15-SEP-1999; 99US-0153995.

XX PA (MONS) MONSANTO CO.

XX PI Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;

XX DR WPI; 2001-281518/29.

XX DR N-PSDB; AAS02487.

XX PT Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
 and the polynucleotides that encode them, useful for increasing the
 insect resistance of plant -

XX PS Claim 5; Page 163-164; 173pp; English.

XX CC The sequence represents a B. thuringiensis Lepidopteran-active
 delta-endotoxin, crystal protein CryET73. The Lepidopteran-active B.
 thuringiensis delta-endotoxin polypeptides may be used as compositions
 that are applied to plant crops to protect them from insect damage. The
 polynucleotides may be used in the production of transgenic plants that
 express the insecticidal polypeptides and consequently have improved
 insect resistance compared to non-transformed plants. Monocotyledonous or
 dicotyledonous plants may be protected in this way, for example corn,
 wheat, soybean, oat, cotton, rice, yam, sorghum, sugarcane, tomato,
 tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
 fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
 cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
 cotton leaf perforator and spruce budworm) may be affected by application
 of the insecticidal polypeptides (full details given in specification).

XX SQ Sequence 625 AA;

Query Match 77.9%; Score 2582.5; DB 22; Length 625;

Best Local Similarity 80.7%; Pred. No. 5.3e-200;

Matches 503; Conservative 44; Mismatches 65; Indels 11; Gaps 6;

Qy 1 MNNVNNGRITTCIDAYNVVAHDPFSEHKSLDTIRKEWMEKRTDHSLYVAPIVGTVSSP 60

Db 1 MNTVNNGRNTTCHANNVVAHDPFSEHKSLNTIEKEWKEKRTDHSLYVAPIVGTVGSF 60

Qy 61 LLKKVGLIGKRILSELWGLIPFSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELEG 120

Db 61 LLKKVGLSVGRILSELQNLIPFSGSIDLMQELIRATEQFINQLNADTLGRVNAELAGL 120

Qy 121 QANIRENQVDNPLNPTQNPVPLSITSSVNTMQOLFNLRLPQFVQGYQLLLPLPAQA 180

Db 121 QANVAEFNRQVDNPLNPNQNPVPLAIDSNTLQQLFLSLRPLQFQIQGYQLLLPLPAQA 180

Qy 181 ANMHLSPFRDVLNADWEGISAATLRTYQNYLKNVTTYEYSNYCINTYQTAFRLNTRLHD 240

Db 181 ANLHLSFIRDVLNADWEGISAATVTRYDRHLNFTRDYSNYCINTYQTAFRLNTRLHD 240

Qy 241 MLEFRTYMLNVEFYVSIWLSFKYQSLVSSGANLYASGSGP--TQSFTHNWFYLSLF 300

Db 241 MLEFRTYMLNVEFYVSIWLSFKYQSLVSSGANLYASGSGP--TQSFTHNWFYLSLF 298

Qy 301 QVNSNYLVNGFSGARLTQTFPNIGGLPGTTTHALLAARVNSYSGVSSGDIG-AVFNQNF 359

Db 299 QVNSNYLVNGLSGARTTITFPNIGGLPGSTTTQTLHFARINRYRGVSSSRIGQANLNQNF 358

Qy 360 SCSTFLPPLTPFVRSWLDSDRGVNTVNTWOTESFESTLGRCCGAFARGNSYFPD 419

Db 359 NISTLFPNLPQTFPIRSWLDSDRGVNTVNTWOGSAFETTL-LRFSIFSARGNSYFPD 417

Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSTGPGGLRAYMVSVHNRKNNIYAVHEN 479

RESULT 15
AAP81356

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OM protein - protein search, using sw model

Run on: December 12, 2003, 16:15:20 ; Search time 21 Seconds
(without alignments)
1273.355 Million cell updates/sec

Title: US-10-040-906A-2
Perfect score: 3314
Sequence: 1 MNVLNGRTTICDAYNVVA.....GTQFELNMVFNPLPIY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/1aa/5A COMB.pap:*
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3: /cgn2_6/ptodata/1/1aa/6A COMB.pap:*
4: /cgn2_6/ptodata/1/1aa/6B COMB.pap:*
5: /cgn2_6/ptodata/1/1aa/PTUS COMB.pap:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3043.5	91.8	634	4	US-09-186-002-12
2	3015.5	91.0	635	3	US-09-041-991A-4
3	3015.5	91.0	635	4	US-09-608-533A-4
4	3010.5	90.8	633	4	US-09-186-002-18
5	3005.5	90.7	634	4	US-09-186-002-2
6	2914.5	87.9	633	3	US-09-041-991A-10
7	2914.5	87.9	633	4	US-09-608-533A-10
8	2913.5	87.9	633	3	US-09-041-991A-8
9	2913.5	87.9	633	4	US-09-608-533A-8
10	2610.5	78.8	623	3	US-09-041-991A-6
11	2610.5	78.8	623	4	US-09-608-533A-6
12	1080	32.6	706	3	US-09-408-820-2
13	336.5	10.2	644	3	US-08-793-331-7
14	327.5	9.9	648	3	US-08-286-870A-4
15	327.5	9.9	719	3	US-08-286-870A-8
16	311.5	9.4	1156	4	US-09-002-285-72
17	311.5	9.4	1156	4	US-09-589-477-72
18	307	9.3	1157	2	US-08-532-547-5
19	307	9.3	1157	2	US-08-379-656B-5
20	307	9.3	1157	3	US-08-455-838-5
21	307	9.3	1157	3	US-09-019-809-5
22	307	9.3	1157	3	US-09-471-177-5
23	306	9.2	1138	1	US-07-973-320-2
24	306	9.2	1138	1	US-07-973-320-4
25	305.5	9.2	643	3	US-09-178-252-25
26	305.5	9.2	1186	3	US-09-178-252-23
27	305.5	9.2	1227	1	US-08-448-170-8

28	305.5	9.2	1227	3	US-08-961-803-9	Sequence 9, Appli
29	304.5	9.2	625	2	US-08-532-547-7	Sequence 7, Appli
30	304.5	9.2	625	2	US-08-532-547-9	Sequence 9, Appli
31	304.5	9.2	625	3	US-09-019-809-7	Sequence 7, Appli
32	304.5	9.2	625	3	US-09-019-809-9	Sequence 9, Appli
33	304.5	9.2	625	4	US-09-471-177-7	Sequence 7, Appli
34	304.5	9.2	625	4	US-09-471-177-9	Sequence 9, Appli
35	294.5	8.9	1176	1	US-08-434-823-2	Sequence 2, Appli
36	294.5	8.9	1176	1	US-08-457-366-2	Sequence 2, Appli
37	293.5	8.9	1229	1	US-08-100-709-4	Sequence 4, Appli
38	293.5	8.9	1229	1	US-08-176-865-4	Sequence 4, Appli
39	293.5	8.9	1229	1	US-08-474-038-4	Sequence 4, Appli
40	293.5	8.9	1229	2	US-08-779-046-4	Sequence 4, Appli
41	293.5	8.9	1229	2	US-08-881-340-4	Sequence 4, Appli
42	292	8.8	488	1	US-08-448-170-10	Sequence 10, Appl
43	292	8.8	488	3	US-08-961-803-10	Sequence 10, Appl
44	291.5	8.8	1179	1	US-08-040-751-1	Sequence 1, Appli
45	288.5	8.7	1176	1	US-07-828-788A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-186-002-12
; Sequence 12, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: delta-Endotoxins
; CURRENT APPLICATION NUMBER: US/09/186.002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-186-002-12

Query Match 91.8%; Score 3043.5; DB 4; Length 634;
Best Local Similarity 90.7%; Pred. No. 1.4e-262;
Matches 573; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

Qy 2 NVVLNGRTTICDAYNVVAHDPPSEHKSLDITRKEMWKRTHDSLYVAPVGVTSFL 61
Db 3 NVVLNGRTTICDAYNVVAHDPPSEHKSLDITRKEMWKRTHDSLYVAPVGVTSFL 62
Qy 62 LKKGSLIGKRIISLWGLIFPPSGSTNLMODILRETEQFLNRLNTDTLARVNAELGLQ 121
Db 63 LKKGSLIGKRIISLWGLIFPPSGSTNLMODILRETEQFLNRLNTDTLARVNAELGLQ 122
Qy 122 ANIREFQQVDNLFNLTQNPVPLSITSSVNTMQQLNRLPQPRVQVQVQLLLPLFAQA 181
Db 123 ANIREFQQVDNLFNLTQNPVPLSITSSVNTMQQLNRLPQPRVQVQVQLLLPLFAQA 182
Qy 182 NMHLSFRDVLNADWEGISAATLRTYQNYLKNVTTEYSNYCINTYQTAFLNRLHDM 241
Db 183 NMHLSFRDVLNADWEGISAATLRTYQNYLKNVTTEYSNYCINTYQTAFLNRLHDM 242
Qy 242 LEPTTYFLNVEFVYSIWSLKFQYSLVSSGANLYASGGPQQTQSTSDWPFYSLFQ 301
Db 243 LEPTTYFLNVEFVYSIWSLKFQYSLVSSGANLYASGGPQQTQSTSDWPFYSLFQ 302
Qy 302 VNSNYLVNGFSGARLTQTFPNIGLPGTTTTTHALLAARVNSYSGVSSGDIQAV-FNQNFS 360
Db 303 VNSNYLVNGFSGARLTQTFPNIGLPGTTTTTHALLAARVNSYSGVSSGDIQAV-FNQNFS 362
Qy 361 CSTFLPPLLPFFVRSWLDGSDRGGVNTVNWQTESPESTLGLRCGTAFTARGNSNPPDY 420
Db 362 CSTFLPPLLPFFVRSWLDGSDRGGVNTVNWQTESPESTLGLRCGTAFTARGNSNPPDY 420

Db 363 CSTVLPPLSTPVRSLWDSGTDREGVATSNWQTESFQTTLRLRCGAFSARGNSNYFPDY 422
Qy 421 FTRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 423 FTRNIGVPLVVRNEDLRPLHYNQIRNIESPSGTPGGLRAYMVSVHNRKNNIYAAENG 482
Qy 481 TMHILAPEDYTGFTTSPHATOVNNOCTRTFISEKFGNOGDSLRFEQSNNTTARYTLRGNGN 540
Db 483 TMHILAPEDYTGFTTSPHATOVNNOCTRTFISEKFGNOGDSLRFEQSNNTTARYTLRGNGN 542
Qy 541 SYNLYRVSLSGNSIRTVINGRVYTAGSNVNTTNDGVNDGNGARFGLDINNMGNVVASDNT 600
Db 543 SYNLYRVSLSGNSIRTVINGRVYTAGSNVNTTNDGVNDGNGARFGLDINNMGNVVASDNT 602
Qy 601 NVPLDINTVNSGTQFELMNMIMFVPTNLPIY 632
Db 603 NVTLIDINTVNSGTQFELMNMIMFVPTNLPIY 634

RESULT 2

US-09-041-991A-4
; Sequence 4, Application US/09041991A
; Patent No. 6107278
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,991A
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-709
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-991A-4

Query Match 91.0%; Score 3015.5; DB 3; Length 635;
Best Local Similarity 90.2%; Pred. No. 4.3e-260;
Matches 573; Conservative 30; Mismatches 29; Indels 3; Gaps 2;
Qy 1 MNVNLNGRTTICDAYNVVAHDPFSEKSLDTIRKEWMEKRTDHSLYVAPIGVTVSSF 60
Db 1 MNVNLNGRTTICDAYNVVAHDPFSEKSLDTIRKEWMEKRTDHSLYVAPIGVTVSSF 60
Qy 61 LLKKVGSLLIGKRLSELWGLIPFSGSTNLMDILRETFQNLQRINTDTLARNVAEGL 120
Db 61 LLKKVGSLLIGKRLSELWGLIPFSGSTNLMDILRETFQNLQRINTDTLARNVAEGL 120

Qy 121 QANIRENQVDNFLNPTQNPVPLSTSSVNTMOOLFNLRLPOFRVOGYQLLLPLPAQA 180
Db 121 QANIRENQVDNFLNPTQNPVPLSTSSVNTMOOLFNLRLPOFRVOGYQLLLPLPAQA 180
Qy 181 ANMELSFTRDVLNADWEGISAAATLRYQYKLYNTTYSNYCINTYTQAFRGLNTRLHD 240
Db 181 ANMELSFTRDVLNADWEGISAAATLRYQYKLYNTTYSNYCINTYTQAFRGLNTRLHD 240
Qy 241 MLEPRTYMFNLVFPYVSIWLSFKYQSLLVSSGANLYASGGPQQTQSTSDWPFLYSLF 300
Db 241 MLEPRTYMFNLVFPYVSIWLSFKYQSLLVSSGANLYASGGPQQTQSTSDWPFLYSLF 300
Qy 301 QVNSNYLVNFGSGARLTQCTPNIGLPGCTTTTHALLAARVNYSGVSGDYGAV-FNQN 359
Db 301 QVNSNYLVNFGSGARLTQCTPNIGLPGCTTTTHALLAARVNYSGVSGDYGAV-FNQN 359
Qy 360 SCSTFPLPLLTFFVRSLWDSGDRGGVNTVNMOTESFESTLGLRCGA--FTARGNSNYF 417
Db 360 SCSTFPLPLLTFFVRSLWDSGDRGGVNTVNMOTESFESTLGLRCGA--FTARGNSNYF 417
Qy 361 NCSTVLPPLSTPFFVRSLWDSGDRGGVNTVNMOTESFESTLGLRCGA--FTARGNSNYF 420
Db 361 NCSTVLPPLSTPFFVRSLWDSGDRGGVNTVNMOTESFESTLGLRCGA--FTARGNSNYF 420
Qy 418 PDYFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVH 477
Db 421 PDYFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAAH 480
Qy 478 ENGTMIHLAPEDYTGFTTSPHATOVNNOCTRTFISEKFGNOGDSLRFEQSNNTTARYTLRG 537
Db 481 ENGTMIHLAPEDYTGFTTSPHATOVNNOCTRTFISEKFGNOGDSLRFEQSNNTTARYTLRG 540
Qy 538 NGSYNLYRVSLSGNSIRTVINGRVYTAGSNVNTTNDGVNDGNGARFGLDINNMGNVVAS 597
Db 541 NGSYNLYRVSLSGNSIRTVINGRVYTAGSNVNTTNDGVNDGNGARFGLDINNMGNVVAS 597
Qy 598 DNTNVPLDINTVNSGTQFELMNMIMFVPTNLPIY 632
Db 601 DNTNVPLDINTVNSGTQFELMNMIMFVPTNLPIY 635

RESULT 3

US-09-608-533A-4
; Sequence 4, Application US/09608533A
; Patent No. 6534644
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/608,533A
; FILING DATE: 30-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041,991
; FILING DATE: 13-MARCH-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-709D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-608-533A-4

Query Match 91.0%; Score 3015.5; DB 4; Length 635;
Best Local Similarity 90.2%; Pred. No. 4.3e-260;
Matches 573; Conservative 30; Mismatches 26; Indels 3; Gaps 2;
QY 1 MNNVLNNGRTTICDAYNVVAHDPPSFPEHKS LDTIRKEMWKRDTDHSLYVAPIVGTVSSP 60
DB 1 MNNVLNNGRTTICDAYNVVAHDPPSFPEHKS LDTIRKEMWKRDTDHSLYVAPIVGTVSSP 60
QY 61 LLKKVGS LIGKRIILSELNGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLDRVNAELEG 120
DB 61 LLKKVGS LIGKRIILSELNGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLDRVNAELEG 120
QY 121 QANIREFQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFVQGYQLLLPLPAQA 180
DB 121 QANIREFQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFVQGYQLLLPLPAQA 180
QY 181 ANMHLSPFIRVDVLNADWEGISAATLRTYQNYLKNYTTSEYNYCINTYQTAFRGLNTRLHD 240
DB 181 ANMHLSPFIRVDVLNADWEGISAATLRTYQNYLKNYTTSEYNYCINTYQTAFRGLNTRLHD 240
QY 241 MLEFRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSTQDWPFYLSLF 300
DB 241 MLEFRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSTQDWPFYLSLF 300
QY 301 QVNSNYLVNGFSGARLTQTFPNIGLPGSTTTTHALLAARVNYSGVSSGDIAGVFNQNF 359
DB 301 QVNSNYLVNGFSGARLTQTFPNIGLPGSTTTTHALLAARVNYSGVSSGDIAGVFNQNF 360
QY 360 SCSTFLPPLLPFVRSWLDSDGSGVNTVNTWQTESPESTLGLRCGA--FTARGNSNYF 417
DB 361 NCSTVLPPLLPFVRSWLDSDGSGVNTVNTWQTESPESTLGLRCGAFFSARGNSNYF 420
QY 418 PDYFIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVH 477
DB 421 PDYFIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAAH 480
QY 478 ENGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNTTARYTLRG 537
DB 481 ENGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNTTARYTLRG 540
QY 538 NGNSNYLVRSVSSLGNSITRTVINGRVYTAGNVNTTNNNDGVNDNGARFLDINNMGVVAS 597
DB 541 NGNSNYLVRSVSSLGNSITRTVINGRVYTAGNVNTTNNNDGVNDNGARFSDINIGNVVAS 600
QY 598 DNTVPLDINTVNSGTOFELMNMIMFVPTNLPPIY 632
DB 601 DNTVPLDINTVNSGTOFELMNMIMFVPTNLPPIY 635

RESULT 4
US-09-186-002-18
; Sequence 18, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186.002
; CURRENT APPLICATION NUMBER: US/09/186.002B
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 18
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-186-002-18
Query Match 90.8%; Score 3010.5; DB 4; Length 633;
Best Local Similarity 89.7%; Pred. No. 1.2e-259;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;
QY 1 MNNVLNNGRTTICDAYNVVAHDPPSFPEHKS LDTIRKEMWKRDTDHSLYVAPIVGTVSSP 60
DB 1 MNNVLNNGRTTICDAYNVVAHDPPSFPEHKS LDTIRKEMWKRDTDHSLYVAPIVGTVSSP 60
QY 61 LLKKVGS LIGKRIILSELNGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLDRVNAELEG 120
DB 61 LLKKVGS LIGKRIILSELNGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLDRVNAELEG 120
QY 121 QANIREFQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFVQGYQLLLPLPAQA 180
DB 121 QANIREFQQVDNLFNPTQNPVPLSITSSVNTMQQLFLNRLPQFVQGYQLLLPLPAQA 180
QY 181 ANMHLSPFIRVDVLNADWEGISAATLRTYQNYLKNYTTSEYNYCINTYQTAFRGLNTRLHD 240
DB 181 ANMHLSPFIRVDVLNADWEGISAATLRTYQNYLKNYTTSEYNYCINTYQTAFRGLNTRLHD 240
QY 241 MLEFRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSTQDWPFYLSLF 300
DB 241 MLEFRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSTQDWPFYLSLF 300
QY 301 QVNSNYLVNGFSGARLTQTFPNIGLPGSTTTTHALLAARVNYSGVSSGDIAGVFNQNF 359
DB 301 QVNSNYLVNGFSGARLTQTFPNIGLPGSTTTTHALLAARVNYSGVSSGDIAGVFNQNF 360
QY 360 SCSTFLPPLLPFVRSWLDSDGSGVNTVNTWQTESPESTLGLRCGAFFSARGNSNYF 419
DB 361 NCSTFLPPLLPFVRSWLDSDGSGVNTVNTWQTESPESTLGLRCGAFFSARGNSNYF 420
QY 420 YFIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVH 479
DB 421 YFIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVH 480
QY 480 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNTTARYTLRG 539
DB 481 GTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNTTARYTLRG 540
QY 540 NSYNLYRVSSLGNSITRTVINGRVYTAGNVNTTNNNDGVNDNGARFLDINNMGVVAS 599
DB 541 NSYNLYRVSSLGNSITRTVINGRVYTAGNVNTTNNNDGVNDNGARFSDINIGNVVAS 600
QY 600 TNPVPLDINTVNSGTOFELMNMIMFVPTNLPPIY 632
DB 601 SDVPLDINTVNSGTOFELMNMIMFVPTNLPPIY 633

RESULT 5
US-09-186-002-2
; Sequence 2, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186.002
; CURRENT APPLICATION NUMBER: US/09/186.002B
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis

US-09-186-002-2

Query Match 90.7%; Score 3005.5; DB 4; Length 634;
Best Local Similarity 89.7%; Pred. No. 3.3e-259;
Matches 567; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

QY 2 NNVLNNGRTTICDAYNVVAHDPEFSEHKS LDTIRKEMWKR TDHSLYVAPIVGT VSSFL 61
DB 3 NSVLNNGRTTICDAYNVVAHDPEFSEHKS LDTIRKEMWKR TDHSLYVAPIVGT VASFL 62
QY 62 LKKVGLIGKRLSELNGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEG 121
DB 63 LKKVGLIGKRLSELNGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEG 122
QY 122 ANIRENQVDNPLNTQNPVLSITSSVNTMOQLFLNRLPQFRVQGLLLPLFAQA 181
DB 123 ANVEEFNRQVDNPLNPNRAVLSITSSVNTMOQLFLNRLPQFRVQGLLLPLFAQA 182
QY 182 NMHLSFIRDVLNADWEGISAATLRTYQNLKNTTYSNYCINTYQTAERGLNRLHDM 241
DB 183 NMHLSFIRDVLNADWEGISAATLRTYQNLKNTTYSNYCINTYQTAERGLNRLHDM 242
QY 242 LBFRTYMFNLNVEYVSIWLSFKYQSLLVSSGANLYASGGPQQTQSFTSQDWPFYLSLFQ 301
DB 243 LBFRTYMFNLNVEYVSIWLSFKYQSLLVSSGANLYASGGPQQTQSFTSQDWPFYLSLFQ 302
QY 302 VNSNTVNLGFSGARLTOTFPNIGGLPGTTTHALLAARVNVSGVSSGDIGA -VFNQNF 360
DB 303 VNSNTVNLGFSGARLSNTFPNIGGLPGTTTHALLAARVNVSGVSSGDIGA -VFNQNF 362
QY 361 CSTFLPPLLTTPVRSWLDGSDRGVNTVNNQTESFESTLGRCGAFTARGNSYFPDY 420
DB 363 CSTFLPPLLTTPVRSWLDGSDRGVNTVNNQTESFESTLGRCGAFTARGNSYFPDY 422
QY 421 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPGTGGGLRAYVSVHNRKNNIYAVHENG 480
DB 423 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPGTGGGLRAYVSVHNRKNNIYAVHENG 482
QY 481 TMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGNQGDSLRFPQSNTTARYTLRGNG 540
DB 483 SMIHLAPNDYGTFTISPIHATQVNNQTRTFISEKFGNQGDSLRFPQSNTTARYTLRGNG 542
QY 541 SYNLYRVSSLGNSIRTVINGRVYASVNTTNNNDGVNDNGARFLDINMGVNASDN 600
DB 543 SYNLYRVSSLGNSIRTVINGRVYASVNTTNNNDGVNDNGARFLDINMGVNASDN 602
QY 601 NVPLDINTVNSGTQFELNMIMFVPTNLPIY 632
DB 603 DVPLDINTVNSGTQFELNMIMFVPTNLPIY 634

RESULT 6

US-09-041-991A-10
; Sequence 10, Application US/09041991A
; Patent No. 6107278
; GENERAL INFORMATION:
; APPLICANT: Schneck, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,991A
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-709
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-041-991A-10

Query Match 87.9%; Score 2914.5; DB 3; Length 633;
Best Local Similarity 87.0%; Pred. No. 4.3e-251;
Matches 551; Conservative 44; Mismatches 37; Indels 1; Gaps 1;

QY 1 MNVLNNGRTTICDAYNVVAHDPEFSEHKS LDTIRKEMWKR TDHSLYVAPIVGT VSSSF 60
DB 1 MNVLNNGRTTICDAYNVVAHDPEFSEHKS LDTIRKEMWKR TDHSLYVAPIVGT VASFF 60
QY 61 LKKVGLIGKRLSELNGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEG 120
DB 61 LKKVGLIGKRLSELNGLIFPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEG 120
QY 121 QANIRENQVDNPLNTQNPVLSITSSVNTMOQLFLNRLPQFRVQGLLLPLFAQA 180
DB 121 QANVEEFNRQVDNPLNPNRAVLSITSSVNTMOQLFLNRLPQFRVQGLLLPLFAQA 180
QY 181 NMHLSFIRDVLNADWEGISAATLRTYQNLKNTTYSNYCINTYQTAERGLNRLHDM 240
DB 181 NMHLSFIRDVLNADWEGISAATLRTYQNLKNTTYSNYCINTYQTAERGLNRLHDM 240
QY 241 MLEFRTYMFNLNVEYVSIWLSFKYQSLLVSSGANLYASGGPQQTQSFTSQDWPFYLSLF 300
DB 241 MLEFRTYMFNLNVEYVSIWLSFKYQSLLVSSGANLYASGGPQQTQSFTSQDWPFYLSLF 300
QY 301 QVNSNTVNLGFSGARLTOTFPNIGGLPGTTTHALLAARVNVSGVSSGDI -GAVFNQNF 359
DB 301 QVNSNTVNLGFSGARLSFTTTPNIGGLPGTTTHALLAARVNVSGVSSGDI -GAVFNQNF 360
QY 360 SCSTFLPPLLTTPVRSWLDGSDRGVNTVNNQTESFESTLGRCGAFTARGNSYFPD 419
DB 361 NCNTISPLSTSFVRSWLDGSDRGVNTVNNQTESFESTLGRCGAFTARGNSYFPD 420
QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPGTGGGLRAYVSVHNRKNNIYAVHENG 479
DB 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPGTGGGLRAYVSVHNRKNNIYAVHENG 480
QY 480 GTMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGNQGDSLRFPQSNTTARYTLRGNG 539
DB 481 GTMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGNQGDSLRFPQSNTTARYTLRGNG 540
QY 540 NSYNLYRVSSLGNSIRTVINGRVYASVNTTNNNDGVNDNGARFLDINMGVNASDN 599
DB 541 NSYNLYRVSSLGNSIRTVINGRVYASVNTTNNNDGVNDNGARFLDINMGVNASDN 600
QY 600 TNVPLDINTVNSGTQFELNMIMFVPTNLPIY 632
DB 601 SDVPLDINTVNSGTQFELNMIMFVPTNLPIY 633

RESULT 7

US-09-533A-10
; Sequence 10, Application US/09608533A
; Patent No. 653464

	GENERAL INFORMATION:	
	APPLICANT: Schnepf, H. Ernest	
	Narva, Kenneth E.	
	Muller-Cohn, Judy	
	TITLE OF INVENTION: Toxins Active Against Pests	
	NUMBER OF SEQUENCES: 10	
	CORRESPONDENCE ADDRESS:	
	ADDRESSES: Saliwanchik, Lloyd & Saliwanchik	
	STREET: 2421 N.W. 41st Street, Suite A-1	
	CITY: Gainesville	
	STATE: Florida	
	COUNTRY: USA	
	ZIP: 32606	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Floppy disk	
	COMPUTER: IBM PC compatible	
	OPERATING SYSTEM: PC-DOS/MS-DOS	
	SOFTWARE: PatentIn	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US 09/041,991	
	FILING DATE: 13-MARCH-1998	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Sanders, Jay M.	
	REGISTRATION NUMBER: 39,355	
	REFERENCE/DOCKET NUMBER: MA-709D1	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (352) 375-8100	
	TELEFAX: (352) 372-5800	
	INFORMATION FOR SEQ ID NO: 10:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 633 amino acids	
	TYPE: amino acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	MOLECULE TYPE: peptide	
	SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
	US-09-608-533A-10	
	Query Match 87.9%; Score 2914.5; DB 4; Length 633;	
	Best Local Similarity 87.0%; Pred. No. 4.3e-251;	
	Matches 551; Conservative 44; Mismatches 37; Indels 1; Gaps 1;	
QY	1 MNVLNNGRTTTCDAYNVVAHDPFPSEKSLDTIRKEWMEWKTDHLSLYVAPIGVTVSSP 60	
DB	1 MNVLNNGRTTTCDAYNVVAHDPFPSEKSLDTIRKEWMEWKTDHLSLYVAPIGVTVASF 60	
QY	61 LKKVGSLIGKRILSELWGILPPSGSTNLMDILRETFQFLNRINTDTTLARVNAEGL 120	
DB	61 LKKUGSLIGKRILSELRLNIIPSGSTNLMDILRETKFLNQKLNTDTLRSVNAETGL 120	
QY	121 QANIREFNQOVDFNLPTONPVPLSITSVNTMQQLFLNRLPQPRVOGYQLLLPLFAQA 180	
DB	121 QANVEFNQRVDNFLPNRNVPLSITSVNTMQQLFLNRLSQFMQGYQLLLPLFAQA 180	
QY	181 ANMHLSPFRDVVLNADWEGISAATRTYQNLYKNVTTEYSNYCINTYTAFRGINTRIHD 240	
DB	181 ANIHLSYRDVLNAAEWGISAATRTYQNHLNRYTRDSNYCIDTYQTAFRGINTRIHD 240	
QY	241 MLEFRTYMLNFYEVVSWSLFKYQSLLVSSGANLYASGSGPQQTSQSDWPFLXSLF 300	
DB	241 MLEFRTYMLNFYEVVSWSLFKYQSLLVSSGANLYASGSGPQQTQTSQDWFLXSLF 300	
QY	301 QVNSNYVLNGFGSGLRTOTFFPNIGLPCTTTTHALLAARVNSYSGVSSGDI - GAVFNQNF 359	
DB	301 QVNSNYVLNGFGSGLSFTTFPNIGLPCTTTTQALLAARVNSYSGGITSGSIGSNFQNF 360	
QY	360 SCSTFLPLLITPFVRSWLDSGDRGVNTVTNWQTESFESTLGRCGAFTARGNSNTPPD 419	
DB	361 NCNTISPLISTSFVRSWLDSGDRGVNTVTNWQTESFESTSGRCGAFTPRGNSNYPG 420	

QY	420 YFIRNISGVPLVVRNEDLERPLHYNEIRNIESPSGTGGCLRAYMVSVNRRKNNIYAVHEN 479
DB	421 YFIRNISGVSLVLRNEDLKRPPLYNEKRNIESPSGTGGCARAYMYSVNKKNNIYAVHEN 480
QY	480 GTMIHLAPEDTGFTISPIHATOVANNQTRTFISEKFGNQDSLRFEQSNNTARYTLRGNG 539
DB	481 GTMIHLAPEDNTGFTISPISHATOVANNQTRTFISEKFGNQDSLRFEQSNNTARYTLRGNG 540
QY	540 NSYNLYRVSSLGNSITRVINGRVYVASNNVNTTNNDGVNDNGARFLDINNGNVVASN 599
DB	541 NSYNLYRVSSIGNSTIRVTINGRVYVASNNVNTTNNDGVNDNGARFSDINIGNVVASN 600
QY	600 TNVPDLINTVNSGTQFELMNIMFVPTNLPIY 632
DB	601 SDVPLDINTVNSGTQFDLMNIMLVPTNISPLY 633
	RESULT 8
	US-09-041-991A-8
	; Sequence 8, Application US/09041991A
	; Patent No. 6107278
	; GENERAL INFORMATION:
	; APPLICANT: Schnepf, H. Ernest
	; APPLICANT: Narva, Kenneth E.
	; APPLICANT: Muller-Cohn, Judy
	; TITLE OF INVENTION: Toxins Active Against Pests
	; NUMBER OF SEQUENCES: 10
	; CORRESPONDENCE ADDRESS:
	; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
	; STREET: 2421 N.W. 41st Street, Suite A-1
	; CITY: Gainesville
	; STATE: Florida
	; COUNTRY: USA
	; ZIP: 32606
	; COMPUTER READABLE FORM:
	; MEDIUM TYPE: Floppy disk
	; COMPUTER: IBM PC compatible
	; OPERATING SYSTEM: PC-DOS/MS-DOS
	; SOFTWARE: PatentIn
	; CURRENT APPLICATION DATA:
	; APPLICATION NUMBER: US/09/041,991A
	; FILING DATE: 13-MAR-1998
	; CLASSIFICATION: 514
	; ATTORNEY/AGENT INFORMATION:
	; NAME: Sanders, Jay M.
	; REGISTRATION NUMBER: 39,355
	; REFERENCE/DOCKET NUMBER: MA-709
	; TELECOMMUNICATION INFORMATION:
	; TELEPHONE: (352) 375-8100
	; TELEFAX: (352) 372-5800
	; INFORMATION FOR SEQ ID NO: 8:
	; SEQUENCE CHARACTERISTICS:
	; LENGTH: 633 amino acids
	; TYPE: amino acid
	; STRANDEDNESS: single
	; TOPOLOGY: linear
	; MOLECULE TYPE: peptide
	; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
	US-09-041-991A-8
	Query Match 87.9%; Score 2913.5; DB 3; Length 633;
	Best Local Similarity 87.2%; Pred. No. 5.3e-251;
	Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;
QY	1 MNVLNNGRTTTCDAYNVVAHDPFPSEKSLDTIRKEWMEWKTDHLSLYVAPIGVTVSSP 60
DB	1 MNVLNNGRTTTCDAYNVVAHDPFPSEKSLDTIRKEWMEWKTDHLSLYVAPIGVTVASF 60
QY	61 LKKVGSLIGKRILSELWGILPPSGSTNLMDILRETFQFLNRINTDTTLARVNAEGL 120
DB	61 LKKUGSLIGKRILSELRLNIIPSGSTNLMDILRETKFLNQKLNTDTLRSVNAETGL 120
QY	121 QANIREFNQOVDFNLPTONPVPLSITSVNTMQQLFLNRLPQPRVOGYQLLLPLFAQA 180

Db 121 QANVEEFNRQVDFNPNRNVAPLSITSSVNTMOQLFLNRLSQFQMGQYQLLLPLFAQA 180
QY 181 ANHLSFTRDVLNADENGISAATLRTYQNYLKNYTTYSYNCINTYQTAFRGLNRLHD 240
Db 181 ANHLSFTRDVLNADENGISAATLRTYQNYLKNYTTYSYNCINTYQTAFRGLNRLHD 240
QY 241 MLEPRTYMLNVEFVYSIWSLFKYOSLLVSSGANLYASGSGPQQTQSTSDWPLYSLF 300
Db 241 MLEPRTYMLNVEFVYSIWSLFKYOSLLVSSGANLYASGSGPQQTQSTSDWPLYSLF 300
QY 301 QVNSNYVLNGFSGARLTOTFPNIGLPGSTTTQALLAARVNSYSGVSSGDI-GAVFNQNF 359
Db 301 QVNSNYVLNGFSGARLTOTFPNIGLPGSTTTQALLAARVNSYSGVSSGDI-GAVFNQNF 359
QY 360 SCSTFLPPLLPFVRSWLDSDGSGVNTVNTWQTESFESTLGRGCGAFTARGNSYPPD 419
Db 361 NCNTISPPLSTSFVRILWLDSDGSGVNTVNTWQTESFESTLGRGCGAFTARGNSYPPG 420
QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYVNSVHNRKNYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYVNSVHNRKNYAVHEN 480
QY 480 GTMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGQSDSLRFEQSNTTARTYLRGNG 539
Db 481 GTMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGQSDSLRFEQSNTTARTYLRGNG 540
QY 540 NSYNLYLRVSSLSGNTSTIRVTINGRVYTTASVNTTNDGNDGNGARFIDINGNVVASDN 599
Db 541 NSYNLYLRVSSLSGNTSTIRVTINGRVYTTASVNTTNDGNDGNGARFIDINGNVVASN 600
QY 600 TNVPLDINVTNSGTOFELMIMFVPTNLPIY 632
Db 601 SDVPLDINVTNLNSGTOFELMIMLVPTNLPLY 633

RESULT 9

US-09-608-533A-8

; Sequence 8, Application US/09608533A

; Patent No. 6534644

; GENERAL INFORMATION:

; APPLICANT: Schnepf, H. Ernest

; Narva, Kenneth E.

; Muller-Cohn, Judy

; TITLE OF INVENTION: Toxins Active Against Pests

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/608,533A

; FILING DATE: 30-Jun-2000

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/041,991

; FILING DATE: 13-MARCH-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Sanders, Jay M.

; REGISTRATION NUMBER: 39,355

; REFERENCE/DOCKET NUMBER: MA-709D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (352) 375-8100

; TELEFAX: (352) 372-5800

; INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-608-533A-8

Query Match 87.9%; Score 2913.5; DB 4; Length 633;

Best Local Similarity 87.2%; Pred. No. 5.3e-251;

Matches 552; Conservative 42; Mismatches 38; Indels 1; Gaps 1;

QY 1 MNVNLNGRITICDAYNVVAHDPPSPHKSILDTTRKEWMEWKRTDHSLYVAPIVGTVSSP 60
Db 1 MNVNLNGRITICDAYNVVAHDPPSPHKSILDTTRKEWMEWKRTDHSLYVAPIVGTVSSP 60
QY 61 LKKGSLIGKRLSELGLIFPSGSLNLMQDIURETEQFLNQLRLNTDTTLARVNAELGL 120
Db 61 LKKGSLIGKRLSELGLIFPSGSLNLMQDIURETEQFLNQLRLNTDTTLARVNAELGL 120
QY 121 QANIREFNQVDNPLNPTQNPVLSITSSVNTMOQLFLNRLSQFQMGQYQLLLPLFAQA 180
Db 121 QANIREFNQVDNPLNPTQNPVLSITSSVNTMOQLFLNRLSQFQMGQYQLLLPLFAQA 180
QY 181 ANHLSFTRDVLNADENGISAATLRTYQNYLKNYTTYSYNCINTYQTAFRGLNRLHD 240
Db 181 ANHLSFTRDVLNADENGISAATLRTYQNYLKNYTTYSYNCINTYQTAFRGLNRLHD 240
QY 241 MLEPRTYMLNVEFVYSIWSLFKYOSLLVSSGANLYASGSGPQQTQSTSDWPLYSLF 300
Db 241 MLEPRTYMLNVEFVYSIWSLFKYOSLLVSSGANLYASGSGPQQTQSTSDWPLYSLF 300
QY 301 QVNSNYVLNGFSGARLTOTFPNIGLPGSTTTQALLAARVNSYSGVSSGDI-GAVFNQNF 359
Db 301 QVNSNYVLNGFSGARLTOTFPNIGLPGSTTTQALLAARVNSYSGVSSGDI-GAVFNQNF 359
QY 360 SCSTFLPPLLPFVRSWLDSDGSGVNTVNTWQTESFESTLGRGCGAFTARGNSYPPD 419
Db 361 NCNTISPPLSTSFVRILWLDSDGSGVNTVNTWQTESFESTLGRGCGAFTARGNSYPPG 420
QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYVNSVHNRKNYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYVNSVHNRKNYAVHEN 480
QY 480 GTMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGQSDSLRFEQSNTTARTYLRGNG 539
Db 481 GTMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGQSDSLRFEQSNTTARTYLRGNG 540
QY 540 NSYNLYLRVSSLSGNTSTIRVTINGRVYTTASVNTTNDGNDGNGARFIDINGNVVASDN 599
Db 541 NSYNLYLRVSSLSGNTSTIRVTINGRVYTTASVNTTNDGNDGNGARFIDINGNVVASN 600
QY 600 TNVPLDINVTNSGTOFELMIMFVPTNLPIY 632
Db 601 SDVPLDINVTNLNSGTOFELMIMLVPTNLPLY 633

RESULT 10

US-09-041-991A-6

; Sequence 6, Application US/09041991A

; Patent No. 6107278

; GENERAL INFORMATION:

; APPLICANT: Schnepf, H. Ernest

; Narva, Kenneth E.

; Muller-Cohn, Judy

; TITLE OF INVENTION: Toxins Active Against Pests

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: Florida

;; COUNTRY: USA
;; ZIP: 32606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/041.991A
;; FILING DATE: 13-MAR-1998
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sanders, Jay M.
;; REGISTRATION NUMBER: 39,355
;; REFERENCE/DOCKET NUMBER: MA-709
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (352) 375-8100
;; TELEFAX: (352) 372-5800
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 623 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-041-991A-6

Query Match 78.8%; Score 2610.5; DB 3; Length 623;
Best Local Similarity 80.3%; Pred. No. 5.2e-224;
Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

Qy 1 MNNVLNCRGTTICDANNVVAHDPSFEHKSIDTIRKEMWKRTHDSLYVAPIVGTVSSP 60
Db 1 MNNVLNCRGTTICDANNVVAHDPSFEHKSIDTIRKEMWKRTHDSLYVAPIVGTVSSP 60
Qy 61 LLKKVGSILGRILSELWGLIFPSGSTNLMQDILRETEQFLNORLNTDTTLARVNAELEG 120
Db 61 LLKKVGSILGRILSELWGLIFPSGSTNLMQDILRETEQFLNORLNTDTTLARVNAELEG 120
Qy 121 QANIREFNOQVDNPLNPTQNPVPLSITSSVNTMQOLFNLRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVAEFNRQVDNPLNPNQNPVPLAIDSNTLQQLFLSRLPQFIQGYQLLLPLFAQA 180
Qy 181 ANHLSFIRVDVLNADENGISAATLRYQNYLKNYTYEYNYCINTYQTAFRGLNTRLHD 240
Db 181 ANHLSFIRVDVLNADENGISAATLRYQNYLKNYTYEYNYCINTYQTAFRGLNTRLHD 240
Qy 241 MLEFRTYMFNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSODWPFYSLF 300
Db 241 MLEFRTYMFNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSODWPFYSLF 300
Qy 241 MLEFRTYMFNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSODWPFYSLF 300
Db 241 MLEFRTYMFNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSODWPFYSLF 300
Qy 301 QVNSNYVLNGFSGARLTOTFPNIGLPGTTHALLAARVNYSGVSSGDIG-AVFNQNF 359
Db 299 QVNSNYVLNGLSGARTTTFNIGLPGSTTQTLHFARINRGVSSSRICQANLNQNF 358
Qy 360 SCSTFLPPLLPFVRSWLDSDRGVNTVNTWQTESPESTLGRCCGTAFTARGNSYPPD 419
Db 359 NISTLFNPLQPFIRSWLDSDGTREGVATSNWQSGAFETTL-LRFSIFSARGNSNFPD 417
Qy 420 YFIRNISQVPLVRNEDLRRLPHYNEIRNIESPSGTPGCLRAYMVSVNHRKNYIAVHEN 479
Db 418 YFIRNISQVGTISNADLARLPHNEIRDI----GTTA--VASLVTVNHRKNYIDTHEN 471
Qy 480 GTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNGQSLRFEQSNNTARTYTLRNG 539
Db 472 GTMHLAPNDYTGFTVSPHATQVNNQTRTFISEKFGNGQSLRFEQSNNTARTYTLRNG 531
Qy 540 NSYNLYLRVSSLSGNTIRVTINGRYVYASNTTNDGVDNGARFLDINMGNVVASDN 599
Db 532 NSYNLYLRVSSLSGNTIRVTINGRYVYTA-NVNTTNDGVDLNGARFSDINMGNVVASN 590
Qy 600 TNVPLDINVTNSGTQFELMNMIMFVPTNPSPLY 623
Db 591 TNVPLDIQVTFNGNPQFELMNMIMFVPTNPSPLY 623

Db 591 TNVPLDIQVTFNGNPQFELMNMIMFVPTNPSPLY 623

RESULT 11
US-09-608-533A-6
; Sequence 6, Application US/09608533A
; Patent No. 6534644
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; Narva, Kenneth E.
; Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/608.533A
; FILING DATE: 30-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041.991
; FILING DATE: 13-MARCH-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-709D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-608-533A-6

Query Match 78.8%; Score 2610.5; DB 4; Length 623;
Best Local Similarity 80.3%; Pred. No. 5.2e-224;
Matches 508; Conservative 46; Mismatches 68; Indels 11; Gaps 6;

Qy 1 MNNVLNCRGTTICDANNVVAHDPSFEHKSIDTIRKEMWKRTHDSLYVAPIVGTVSSP 60
Db 1 MNNVLNCRGTTICDANNVVAHDPSFEHKSIDTIRKEMWKRTHDSLYVAPIVGTVSSP 60
Qy 61 LLKKVGSILGRILSELWGLIFPSGSTNLMQDILRETEQFLNORLNTDTTLARVNAELEG 120
Db 61 LLKKVGSILGRILSELWGLIFPSGSTNLMQDILRETEQFLNORLNTDTTLARVNAELEG 120
Qy 121 QANIREFNOQVDNPLNPTQNPVPLSITSSVNTMQOLFNLRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVAEFNRQVDNPLNPNQNPVPLAIDSNTLQQLFLSRLPQFIQGYQLLLPLFAQA 180
Qy 181 ANHLSFIRVDVLNADENGISAATLRYQNYLKNYTYEYNYCINTYQTAFRGLNTRLHD 240
Db 181 ANHLSFIRVDVLNADENGISAATLRYQNYLKNYTYEYNYCINTYQTAFRGLNTRLHD 240
Qy 241 MLEFRTYMFNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSODWPFYSLF 300
Db 241 MLEFRTYMFNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSODWPFYSLF 300

QY 301 QVNSVNLGSPGARTLTFFNIGLPGTTTTTHALLARVNSGVSSGDIG-AVFNONF 359
 DB 299 QVNSVNLGSGARTTTFNIGLPGSTTTTTHLHARINVRGVSSRIGQANLQNF 358
 QY 360 SCSTPLPPLLPFVRSLWSDSGDRGVNTVNMWQTESPESTLGLRCGAFARGNSNYPPD 419
 DB 359 NISTLFPLOPPIFIRSLWSDSGDRGVATSNWQSGAETTL-LRFSIFSARGNSNFPD 417
 QY 420 YFIRNISGVPLVRNEDLRRLPHYNEIRNISPSGTPGGLRAYVSVNHRKNYIAVHEN 479
 DB 418 YFIRNISGVGTISNADLRLPHNEIRDI-----GTTA--VASLTVNHRKNYIDYHEN 471
 QY 480 GTMHLAPEDYGTFTISPHATOVNNOVRTFTSEKFGNOGSLRPEQSNNTARYTLRGNG 539
 DB 472 GTMHLAPENDYGTFTVSPHATOVNNOVRTFTSEKFGNOGSLRPELSNNTARYTLRGNG 531
 QY 540 NSYNLYLRVSSLSGNTIRVTNGRYVYTAASNVTNTTNDGVNDNGARFLDINMGNVASDN 599
 DB 532 NSYNLYLRVSSLSGNTIRVTNGRYVYTA-NVNTTNDGVNDNGARFSDINMGNVASAN 590
 QY 600 TNVPLDINVTNSGTQFELMNMIMFVPTNLPPIY 632
 DB 591 TNVPLDIQVTFNGNQFELMNMIMFVPTNPSPLY 623

RESULT 12

US-09-408-820-2
 ; Sequence 2, Application US/09408820
 ; Patent No. 6204057
 ; GENERAL INFORMATION:
 ; APPLICANT: Schnetter, Wolfgang
 ; APPLICANT: Krieger, Lutz
 ; APPLICANT: Zhang, Jiaoming
 ; TITLE OF INVENTION: Polynucleotides And The Proteins Encoded Thereby,
 ; TITLE OF INVENTION: Suitable For Controlling Lamellicorn Beetles
 ; FILE REFERENCE: S-30403/A/UHD/CGC1996/PCT
 ; CURRENT APPLICATION NUMBER: US/09/408,820
 ; CURRENT FILING DATE: 1999-09-29
 ; EARLIER APPLICATION NUMBER: 09/051,454
 ; EARLIER FILING DATE: 1998-04-07
 ; EARLIER APPLICATION NUMBER: DE 195 40 223.5
 ; EARLIER FILING DATE: 1995-10-18
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 706
 ; TYPE: PRT
 ; ORGANISM: Bacillus popilliae
 ; FEATURE:
 ; OTHER INFORMATION: strain subspecies: melonlonthae H1; stage of
 ; OTHER INFORMATION: development: spore stage; cell type: sporangium
 ; FEATURE:
 ; OTHER INFORMATION: immediate origin: isolate from the haemolymph of
 ; OTHER INFORMATION: Melonlontha melonlontha individuals captured on open
 ; OTHER INFORMATION: ground
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(706)
 ; OTHER INFORMATION: mature protein crystal peptide determined by
 ; OTHER INFORMATION: experiment
 ; US-09-408-820-2

Query Match 32.6%; Score 1080; DB 3; Length 706;
 Best Local Similarity 38.4%; Pred. No. 1.7e-87;
 Matches 264; Conservative 96; Mismatches 233; Indels 94; Gaps 21;
 QY 2 NNVLNN-----GRTTICDA-----YNVVAHDPFSEHKSLDTIRKEWMEKRTD 45
 DB 58 NNDNNDAICDELGLTPIDNNNTTSTDFTPIVNVRTDP--FRKXSTQBLTREWTEWKENS 115
 QY 46 HSLVAPVIGTVSSPLKKVGLIGKRLISELWGLIPFGSGTSLMQLDILRETEQFLNORL 105
 DB 116 PGLTPAIVGVVTSFLQSLKKQATSFLLKTLTDLFLFNSSLTWEEILRATEQVQERL 175

QY 106 NDTLARVNAELGLEQANIREFNOQVDFNLPTQNPVPLSTISSVNTWQOLFNLRLPOFR 165
 DB 176 DTDTFANVRQSELVGLKNNLTTFNDQVEDFLQNRVGISPLAIDSINTWQOLFVNLRLPOQF 235
 QY 166 VQGVQLLLPLFAAANMHLISFIRDVVLNADWEGISAATLRTYQNLKYNLYTTEYSNYCIN 225
 DB 236 VSGQVQLLLPLFAAATLHLTFLRDVILNADWENIPTAQLNTYTRYKEYTAESNYALS 295
 QY 226 TYQTAFRGLNTR-----LHDMLEFRTYMFLNFEYVSIWSLKFYQSLVSSGANLYASG 279
 DB 296 TYDDGFR--TRFYPRNTLEDMLQKFTMTLNALDLVSIWSLLKYVNLVYSTSANLYNIG 352
 QY 280 SGPOQTSQTSQDWPFLYSLFQVNSVNLNGFSGARLTQTFFPNIGG-----LPGTTTTH 333
 DB 353 DNKYNEGAYPISYGPFFNSYIQTKSNYVLGSGVIGARFTYSTVLGRYHLHDDLKNIIT- 411
 QY 334 ALLARVNSYSGVSSGDIGAVFN-----QNFSCSTFLP-PLLTTP 371
 DB 412 -----YVGGTQGNIGVQLSTTDELKQQAATRDSLVDQFFTLNCLMNPITAP 463
 QY 372 -FVRSWLDG-SDRGGVNTVTNMOTESPESTLGL-RCGAFARGNSNYFPDPIFNISGV 428
 DB 464 YFATSLVESRYSSIGGYLRKDVPKSE--DSTCGLNGPQWTS-----YPDYITNISAT 515
 QY 429 PLVVRNEDLRRLPHYNEIRNIESPSGTPGGLRAYVSVNHRKNYIAVHENGTMHLAPE 488
 DB 516 VQINGENTDTTPLYFKENRPITSTRGV-----NKVIAVYNRKANIAGTNGQTMHQAPP 570
 QY 489 DYTGTFTISPHATOVNNOVRTFTSEKFGNOGSLRPEQSNNTARYTLRGNG-NSNLVLR 547
 DB 571 DGTGFTVSPHPSA--NTITSIKENTGNSGDSLHL-KGQGYLHMLSGNQDRLVLR 627
 QY 548 VSSLGNSSTIRVTNGRYVYTAASNVTNTTNDGVNDNGARFLDINMGN--VVASDNTNVPLD 605
 DB 628 LSGAAN--QIKLQSPITSYAPDTSNNESGIDTNGSKFKDFATSTPPVPEQK-----E 679
 QY 606 INVTFNSGTQFELMNMIMFVPTNLPPIY 632
 DB 680 IVLYFEGVGSLLDMNLIFLPADDTPLY 706

RESULT 13

US-08-793-331-7
 ; Sequence 7, Application US/08793331
 ; Patent No. 6071877
 ; GENERAL INFORMATION:
 ; APPLICANT: DELECLUSE, ARMELE
 ; APPLICANT: THIERY, ISABELLE
 ; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING A TOXIC ACTIVITY AGAINST
 ; TITLE OF INVENTION: INSECTS OF THE DIPTERA FAMILY
 ; FILE REFERENCE: 0660-0116-0 PCT
 ; CURRENT APPLICATION NUMBER: US/08/793,331
 ; CURRENT FILING DATE: 1997-05-13
 ; EARLIER APPLICATION NUMBER: PCT/FR95/01116
 ; EARLIER FILING DATE: 1995-08-24
 ; EARLIER APPLICATION NUMBER: FR 94/10299
 ; EARLIER FILING DATE: 1994-08-25
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 644
 ; TYPE: PRT
 ; ORGANISM: B. thuringiensis ser. israelensis
 ; US-08-793-331-7

Query Match 10.2%; Score 336.5; DB 3; Length 644;
 Best Local Similarity 23.1%; Pred. No. 2.7e-21;
 Matches 167; Conservative 98; Mismatches 257; Indels 201; Gaps 34;
 QY 27 EHKSLDTIRKEWMEKRTDHSLY-----VAP---IVGTVSSPLKKVGLIGKRLISE 76
 DB 3 EDSLDTLSIV---NETDFPLNNYTEPTIAPALIAVAPIAQVLAIGWPAKAAAFSK 58

Db 544 FGDIRVNINPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNR-----GBD 596
Qy 587 LDINMGVNVASDNTNVPDLINVT-----FNSGTQFELMNMIFVPTNL 628
Db 597 LDYKTRTVGTTPPFSFLDVQSTFTTIGAWNFSSGNEVYDRIEFVPEV 645

RESULT 15

US-08-286-870A-8
; Sequence 8, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-8

Query Match 9.9%; Score 327.5; DB 3; Length 719;
Best Local Similarity 22.8%; Pred. No. 2e-20;
Matches 162; Conservative 103; Mismatches 271; Indels 173; Gaps 32;
Qy 21 HDPFSFEHK---SLDTIRKEW-MEWKRTDH-----SLY-VAP----- 52
Db 9 HQSFSSNAKVKISTDSKNETDIELQNINHECLMKSEYENVEPVFSASTIQTGIGIAG 68
Qy 53 -IVGTSSFLKKVGLSKIRLSLWGLIFPGSGTNLMQDILRETEQFLNORLNTDLA 111
Db 69 KILGTLGVPEAGQVASYL-SFILGELW----PKGK-NQWEIFMEHVEIINQKISTYARN 122
Qy 112 RVNALEGLQANIREFNOQVNFNPTONPVLPSIT-SSVNTMQOLFNLRLPQFRVQGY 170
Db 123 KALTDLKGGLDALAVYHDSLESWGVRNNRNRARSVYKSOYIALELMFVQKLPFAVSAGEE 182

Qy 171 LLLPLLEQAARNHLSFIRDVVLNADENGISAATLRTYQNLKNTYTESYCNINTYQTA 230
Db 183 VELLPIYAAQANLHLLLRDASIFGKWLGSSEISITFYNRQVERAGDYSDCHCVKYSTG 242
Qy 231 FRGL-NTRLHMDL--EFRTYMLNVFVYVSWLSFKYQSLIVSSGANL-----YASGSGP 282
Db 243 LNNLFGTNAESWVRYNQFRDMLNVLVALFPSYDTQMPYIKTKTAQLTREYVTDAGT 302
Qy 283 QQTQ-SFTSQDW-----PPL-----YSLFQVNSN-YVLNGFSG 313
Db 303 VHPHPSFTSTTYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMWGG 362
Qy 314 ARLTOTFENICGLPGTTTTTHALLAARVNYSGVSSGDIGAVPNQNFSCSTFLPPLTPPV 373
Db 363 HKL--EFRTIGTGLNIST-----QGSTNTSINPVTLPPT 394
Qy 374 RSWLDSGSDRGVNTVT-----NWO--TESPESTLGLRCGAFARGNSGNYFPD 419
Db 395 SRDVYRTESLAGLNLFTQPVNGVPRVDFHKKFVTHPIAS-----DNFYYPG 441
Qy 420 YFIRNIGVPLVVRNEDLRRPLHYNIEIRNIESPGTGGRLRAYMVSVHNRKNYIA-VHE 478
Db 442 Y-----AGIGTQLQDSNELPPEATGPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494
Qy 479 NGTMHLAPEDYTGFTISPIHATQV-----NNQTRTFISEKFG-NQGDLSLRFESQNTTA 531
Db 495 SA-----DRTN-TIEPNSITQPLVKAFNLSSGAAVVRGPGFTGGDILR--RTNTGT 543
Qy 532 RYTLRGNGN-----SYNLYLRVSSLGNSTIRVTNGRVYVYASNVNTTNDGVNDNGARF 586
Db 544 FGDIRVNINPPFAQRVVRIRVASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596
Qy 587 LDINMGVNVASDNTNVPDLINVT-----FNSGTQFELMNMIFVPTNL 628
Db 597 LDYKTRTVGTTPPFSFLDVQSTFTTIGAWNFSSGNEVYDRIEFVPEV 645

Search completed: December 12, 2003, 16:18:44
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 16:11:40 ; Search time 39 Seconds
(without alignments)
4181.776 Million cell updates/sec

Title: US-10-040-906A-2

Perfect score: 3314

Sequence: 1 MNVNLNGRTTICDAYNVA.....GTOFELNMIMVPTNLPPIY 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3044.5	91.9	633	2 Q8GHF3	Q8GHF3 bacillus th
2	3029.5	91.4	633	2 Q86N5	Q86N5 bacillus th
3	3025.5	91.3	633	2 Q86N4	Q86N4 bacillus th
4	2998.5	90.5	633	2 Q8GH90	Q8GH90 bacillus th
5	2641.5	79.7	551	2 Q8RM89	Q8RM89 bacillus th
6	328.5	9.9	1231	2 Q8KNY2	Q8KNY2 bacillus th
7	327.5	9.9	719	2 Q83NJ5	Q83NJ5 bacillus th
8	325.5	9.8	719	2 Q85796	Q85796 bacillus th
9	323.5	9.8	719	2 Q8KY61	Q8KY61 bacillus th
10	317.5	9.6	719	2 Q8F0B8	Q8F0B8 bacillus th
11	280.5	8.5	1180	2 Q8S5V8	Q8S5V8 bacillus th
12	279.5	8.4	645	2 Q8S603	Q8S603 bacillus th
13	278.5	8.4	1228	2 Q83NM5	Q83NM5 bacillus th
14	277.5	8.4	381	2 Q45740	Q45740 bacillus th
15	276.5	8.3	620	2 Q45720	Q45720 bacillus th
16	276.5	8.3	1176	2 Q45736	Q45736 bacillus th

17	276.5	8.3	1228	2	Q93T75	Q93T75 bacillus th
18	274.5	8.3	1176	2	Q9S514	Q9S514 bacillus th
19	270.5	8.2	1118	2	Q9AM83	Q9AM83 bacillus th
20	270.5	8.2	1176	2	Q9RC30	Q9RC30 bacillus th
21	270	8.1	1177	2	Q8GLY5	Q8GLY5 bacillus th
22	268	8.1	1155	2	Q9F296	Q9F296 bacillus th
23	264.5	8.0	1178	2	Q9R826	Q9R826 bacillus th
24	264	8.0	723	2	Q9S4B5	Q9S4B5 bacillus th
25	264	8.0	1174	2	Q45749	Q45749 bacillus th
26	264	8.0	1177	2	Q03743	Q03743 bacillus th
27	263	7.9	1155	2	Q93T21	Q93T21 bacillus th
28	262.5	7.9	1144	2	Q8KZL7	Q8KZL7 bacillus th
29	262	7.9	638	2	Q87654	Q87654 bacillus th
30	261.5	7.9	1178	2	Q45768	Q45768 bacillus th
31	259	7.8	1177	2	Q45735	Q45735 bacillus th
32	257.5	7.8	1236	2	Q939T3	Q939T3 bacillus th
33	255.5	7.7	618	2	Q32306	Q32306 bacillus th
34	255	7.7	1118	2	Q9AM82	Q9AM82 bacillus th
35	253	7.6	607	2	Q45721	Q45721 bacillus th
36	253	7.6	618	2	Q45737	Q45737 bacillus th
37	250	7.5	652	2	Q9SGN9	Q9SGN9 bacillus th
38	246	7.4	1169	2	Q8GHE8	Q8GHE8 bacillus th
39	244	7.4	1160	2	Q93TF9	Q93TF9 bacillus th
40	237	7.2	650	2	Q8VNX2	Q8VNX2 bacillus th
41	231.5	7.0	1189	2	Q9L877	Q9L877 bacillus th
42	230	6.9	660	2	Q8RQU6	Q8RQU6 bacillus th
43	216	6.5	1144	2	Q45745	Q45745 bacillus th
44	214.5	6.5	1171	2	Q06894	Q06894 bacillus th
45	212	6.4	723	2	Q9EVR2	Q9EVR2 bacillus th

ALIGNMENTS

RESULT 1

Q8GHF3 Q8GHF3 PRELIMINARY; PRT; 633 AA.

AC Q8GHF3;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Insecticidal crystal protein Cry2Aa.

GN Cry2Aa.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Dongbei 66;

RA Wei G., Jie Z., Dafang H., Guoxun L.;

RT "New cry2Aa gene from Chinese native isolates Bt strain Dongbei 66.";

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP252262; AAC13734.1; --

SQ SEQUENCE 633 AA; 70822 MW; 9CA19991B78798A6 CRC64;

Query Match 91.9%; Score 3044.5; DB 2; Length 633;

Best Local Similarity 90.5%; Pred. No. 1e-196;

Matches 573; Conservative 34; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MNVNLNGRTTICDAYNVAHDPPFSEHKSLDTIRKEMWEKTDHSLYVAPVGVTVSSF 60

Db 1 MNVNLNGRTTICDAYNVAHDPPFSEHKSLDTIRKEMWEKTDHSLYVAPVGVTVSSF 60

Qy 61 LLKKVSLGKRLTSLWGLIPSGSTNLMDTLRETEQFLNORLNTDTLARNVAEGL 120

Db 61 LLKKVSLGKRLTSLWGLIPSGSTNLMDTLRETEQFLNORLNTDTLARNVAEGL 120

Qy 121 QANIRFNOQVDNFTNPTNPVPLSTSSVNTMQQLFLNRLPQFRVQGVQLLLPLFAQA 180

Db 121 QANIRFNOQVDNFTNPTNPVPLSTSSVNTMQQLFLNRLPQFRVQGVQLLLPLFAQA 180

Qy 181 ANMHSFIRDVVLNADEWGISAAATLTYQNYLQNYTTEYSNYCINTYQTAFLGNLRLHD 240

Db 181 ANMHSFIRDVVLNADEWGISAAATLTYQNYLQNYTTEYSNYCINTYQTAFLGNLRLHD 240

Db 181 ANHLSFIRDVILNADEWISAAATLRTYDRYLRNVTDRYSNYCINTYQTAFRGLNTRLHD 240
Qy 241 MLEPRTYMLNVPFYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSTSDWPFYLSLF 300
Db 241 MLEPRTYMLNVPFYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSTTAQNWPFLYSLF 300
Qy 301 QVNSNYLVNGPFGSARLTOTFPNIGGLPQTTHALLAARVNYSGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYLVNGPFGSARLTOTFPNIGGLPQTTHALLAARVNYSGVSSGLIGATNLNHNF 360
Qy 360 SCSTFLPPLLPFVRSWLDSDRGVNTVNMQTESFESTLGRCGAFTARGNSNYFPD 419
Db 361 NCSTVLPPLSPFVRSWLDSDRGVNTVNMQTESFESTLGRCGAFTARGNSNYFPD 420
Qy 420 YFIRNIGSVPLVWNEDELRLPLHNEIRNIESPSGTPGGRLAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNIGSVPLVWNEDELRLPLHNEIRNIESPSGTPGGRLAYMVSVHNRKNNIYAAEN 480
Qy 480 GTMIHLAPEDYTGFTISPIHATQVNNOTRPFISEKFGNQGDSLRFEQSNNTARYTLRGNG 539
Db 481 GTMIHLAPEDYTGFTISPIHATQVNNOTRPFISEKFGNQGDSLRFEQSNNTARYTLRGNG 540
Qy 540 NSYNLYLRVSSLGNSITRVINGRVYTSASVNTTNDGVNDNGARFLDINMGVNASDN 599
Db 541 NSYNLYLRVSSLGNSITRVINGRVYTSASVNTTNDGVNDNGARFLDINMGVNASDN 600
Qy 600 TNVPLDINVTNSGTQFELNMIMVPTNLPPIY 632
Db 601 TNVPLDINVTNSGTQFELNMIMVPTNLPPIY 633

RESULT 2

Q9S6N5 PRELIMINARY; PRT; 633 AA.
ID Q9S6N5
AC Q9S6N5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cry2Aa protein.
GN Cry2Aa.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y271;
RA Yu J., Pang Y.;
RT "Cloning and characterisation of insecticidal crystal protein gene
cry2Aa6 from new isolated strain of Bacillus thuringiensis YZ71.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132465; CAAL10672.1; -
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR Pfam; PF03944; endotoxin C; 1.
DR Pfam; PF03945; endotoxin N; 1.
SQ SEQUENCE 633 AA; 70937 MW; CC727E333B75A593 CRC64;

Query Match 91.4%; Score 3029.5; DB 2; Length 633;
Best Local Similarity 90.0%; Pred. No. 1.1e-195;
Matches 570; Conservative 36; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MNVNLNGRTTICDAYNVVAHDPPFSEHKSLDTIRKEMWKRTHSLYVAPIGVTVSSF 60
Db 1 MNVNLNGRTTICDAYNVVAHDPPFSEHKSLDTIRKEMWKRTHSLYVAPIGVTVSSF 60
Qy 61 LLKKVGLIGKRLISELWGLIFPGSGTNLMQDILRETEQFLNQLNRTDTLARVNAEGL 120
Db 61 LLKKVGLIGKRLISELWGLIFPGSGTNLMQDILRETEQFLNQLNRTDTLARVNAEGL 120
Qy 121 QANIREFNQVDNPLNPTONPVLISITSSVNTWQQLFLNPLPFRVQGYQLLLPLFAQA 180
Db 121 QANIREFNQVDNPLNPTONPVLISITSSVNTWQQLFLNPLPFRVQGYQLLLPLFAQA 180

Qy 181 ANHLSFIRDVILNADEWISAAATLRTYDRYLRNVTDRYSNYCINTYQTAFRGLNTRLHD 240
Db 181 ANHLSFIRDVILNADEWISAAATLRTYDRYLRNVTDRYSNYCINTYQTAFRGLNTRLHD 240
Qy 241 MLEPRTYMLNVPFYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSTSDWPFYLSLF 300
Db 241 MLEPRTYMLNVPFYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSTTAQNWPFLYSLF 300
Qy 301 QVNSNYLVNGPFGSARLTOTFPNIGGLPQTTHALLAARVNYSGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYLVNGPFGSARLTOTFPNIGGLPQTTHALLAARVNYSGVSSGLIGATNLNHNF 360
Qy 360 SCSTFLPPLLPFVRSWLDSDRGVNTVNMQTESFESTLGRCGAFTARGNSNYFPD 419
Db 361 NCSTVLPPLSPFVRSWLDSDRGVNTVNMQTESFESTLGRCGAFTARGNSNYFPD 420
Qy 420 YFIRNIGSVPLVWNEDELRLPLHNEIRNIESPSGTPGGRLAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNIGSVPLVWNEDELRLPLHNEIRNIESPSGTPGGRLAYMVSVHNRKNNIYAAEN 480
Qy 480 GTMIHLAPEDYTGFTISPIHATQVNNOTRPFISEKFGNQGDSLRFEQSNNTARYTLRGNG 539
Db 481 GTMIHLAPEDYTGFTISPIHATQVNNOTRPFISEKFGNQGDSLRFEQSNNTARYTLRGNG 540
Qy 540 NSYNLYLRVSSLGNSITRVINGRVYTSASVNTTNDGVNDNGARFLDINMGVNASDN 599
Db 541 NSYNLYLRVSSLGNSITRVINGRVYTSASVNTTNDGVNDNGARFLDINMGVNASDN 600
Qy 600 TNVPLDINVTNSGTQFELNMIMVPTNLPPIY 632
Db 601 TNVPLDINVTNSGTQFELNMIMVPTNLPPIY 633

RESULT 3

Q9S6N4 PRELIMINARY; PRT; 633 AA.
ID Q9S6N4
AC Q9S6N4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cry2Aa protein.
GN Cry2Aa.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL39;
RA Yu J., Pang Y.;
RT "Cloning and characterisation of insecticidal crystal protein gene
cry2Aa5 from new isolated strain of Bacillus thuringiensis SL39.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132464; CAAL10671.1; -
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR Pfam; PF03944; endotoxin C; 1.
DR Pfam; PF03945; endotoxin N; 1.
SQ SEQUENCE 633 AA; 70925 MW; 8FB7F5216AC6F7B8 CRC64;

Query Match 91.3%; Score 3025.5; DB 2; Length 633;
Best Local Similarity 90.0%; Pred. No. 2e-195;
Matches 570; Conservative 35; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MNVNLNGRTTICDAYNVVAHDPPFSEHKSLDTIRKEMWKRTHSLYVAPIGVTVSSF 60
Db 1 MNVNLNGRTTICDAYNVVAHDPPFSEHKSLDTIRKEMWKRTHSLYVAPIGVTVSSF 60
Qy 61 LLKKVGLIGKRLISELWGLIFPGSGTNLMQDILRETEQFLNQLNRTDTLARVNAEGL 120
Db 61 LLKKVGLIGKRLISELWGLIFPGSGTNLMQDILRETEQFLNQLNRTDTLARVNAEGL 120
Qy 121 QANIREFNQVDNPLNPTONPVLISITSSVNTWQQLFLNPLPFRVQGYQLLLPLFAQA 180


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Db 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMOQLFLNRLPQFQIQYQLLLPLFAQA 180
Qy 181 ANHLSFIRDVLNADWEGISAATLRTYQNYLKNYTESNYCINTYQTAFRGLNTRLHD 240
Db 181 ANHLSFIRDVLNADWEGISAATLRTYQNYLKNYTESNYCINTYQTAFRGLNTRLHD 240
Qy 241 MLEFRITMFLNVEYVSWLSFKYQSLVSSGANLYASGGPQOQTSFTSQDWPFYLSLF 300
Db 241 MLEFRITMFLNVEYVSWLSFKYQSLVSSGANLYASGGPQOQTSFTSQDWPFYLSLF 300
Qy 301 QVNSNYVLNGFSGARLTQTTPFNIGGLPGTTHALLAARVNSYGGVSSGGDIGAV-FNQNF 359
Db 301 QVNSNYVLNGFSGARLTQTTPFNIGGLPGTTHALLAARVNSYGGVSSGGDIGAV-FNQNF 360
Qy 360 SCSTFLPPLLTTPFVRSWLDGSDRGVNTVNWQTESFESTLGLRCGAFTARGNSYFPD 419
Db 361 NCSTVLPPLSTPFVRSWLDGSDRGVNTVNWQTESFESTLGLRCGAFTARGNSYFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 480
Qy 480 GTMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGNQDLSLRFESQNTTARYTLRGNG 539
Db 481 GTMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGNQDLSLRFESQNTTARYTLRGNG 540
Qy 540 NSYNLYLRVSSLGNSITRVINGRVYTTASNVTNTNNDGVNDNGARFLDINMGVNASDN 599
Db 541 NSYNLYLRVSSLGNSITRVINGRVYTTASNVTNTNNDGVNDNGARFLDINMGVNASDN 600
Qy 600 TNVPLDINVTNSGTFQELNMIMFVPTNLPPIY 632
Db 601 TNVPLDINVTNSGTFQELNMIMFVPTNLPPIY 633

RESULT 4
Q8GH90 PRELIMINARY; PRT; 633 AA.
AC Q8GH90;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Crystal delta-endotoxin.
GN Crf2AB.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-Pr-88;
RA Li C., Zhang J., Huang D., Li G.;
RT "A crystal endotoxin from Bacillus thuringiensis strain B-Pr-88.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF336115; AA013296.1; -.
FT NON_TER 633 AA; 70726 MW; 01EFA93A35564D01 CRC64;
SQ SEQUENCE 633 AA; 70726 MW; 01EFA93A35564D01 CRC64;

Query Match 90.5%; Score 2998.5; DB 2; Length 633;
Best Local Similarity 89.4%; Pred. No. 1.3e-193;
Matches 566; Conservative 40; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MNNVLNNGRTTICDAYNVVAHDPPSPFHKSLDTIRKEMWETKTDHSLYVAPVIGTVSSF 60
Db 1 MNSVLSNGRTTICDAYNVVAHDPPSPFHKSLDTIRKEMWETKTDHSLYVAPVIGTVSSF 60
Qy 61 LLKKVSLGKRLISELWGLIFPSGSTNLMDILRETEQFLNQLNLTDLARVNAEGL 120
Db 61 LLKKVSLGKRLISELWGLIFPSGSTNLMDILRETEQFLNQLNLTDLARVNAEGL 120
Qy 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMOQLFLNRLPQFQIQYQLLLPLFAQA 180
Db 121 QANVEEFNRQVDNLFNPNRAVPLSITSSVNTMOQLFLNRLPQFQIQYQLLLPLFAQA 180
Qy 181 ANHLSFIRDVLNADWEGISAATLRTYQNYLKNYTESNYCINTYQTAFRGLNTRLHD 240
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Db 181 ANHLSFIRDVLNADWEGISAATLRTYQNYLKNYTESNYCINTYQSAFKGLNTRLHD 240
Qy 241 MLEFRITMFLNVEYVSWLSFKYQSLVSSGANLYASGGPQOQTSFTSQDWPFYLSLF 300
Db 241 MLEFRITMFLNVEYVSWLSFKYQSLVSSGANLYASGGPQOQTSFTSQDWPFYLSLF 300
Qy 301 QVNSNYVLNGFSGARLTQTTPFNIGGLPGTTHALLAARVNSYGGVSSGGDIGA-VFNQNF 359
Db 301 QVNSNYVLNGFSGARLTQTTPFNIGGLPGTTHALLAARVNSYGGVSSGGDIGA-VFNQNF 360
Qy 360 SCSTFLPPLLTTPFVRSWLDGSDRGVNTVNWQTESFESTLGLRCGAFTARGNSYFPD 419
Db 361 NCSTFLPPLLTTPFVRSWLDGSDRGVNTVNWQTESFESTLGLRCGAFTARGNSYFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 480
Qy 480 GTMIHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGNQDLSLRFESQNTTARYTLRGNG 539
Db 481 GSIHLAPNDYGTFTISPIHATQVNNQTRTFISEKFGNQDLSLRFESQNTTARYTLRGNG 540
Qy 540 NSYNLYLRVSSLGNSITRVINGRVYTTASNVTNTNNDGVNDNGARFLDINMGVNASDN 599
Db 541 NSYNLYLRVSSLGNSITRVINGRVYTTASNVTNTNNDGVNDNGARFLDINMGVNASDN 600
Qy 600 TNVPLDINVTNSGTFQELNMIMFVPTNLPPIY 632
Db 601 SDVPLDINVTNSGTFQELNMIMFVPTNLPPIY 633

RESULT 5
Q9RM89 PRELIMINARY; PRT; 551 AA.
AC Q9RM89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cy2A protein (Fragment).
GN CrY2AD.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CY29;
RA Yu J., Fang Y.;
RT "Cloning and characterisation of insecticidal crystal protein gene cry2Ad from new isolated strain of Bacillus thuringiensis CY29.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ132463; CAA10670.2; -.
DR InterPro: IPR005639; endotoxin_N.
DR Pfam: PF03945; endotoxin_N; 1.
FT NON_TER 551
SQ SEQUENCE 551 AA; 62126 MW; D6B77B8AE713E98A CRC64;

Query Match 79.7%; Score 2641.5; DB 2; Length 551;
Best Local Similarity 90.4%; Pred. No. 1.2e-169;
Matches 498; Conservative 30; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MNNVLNNGRTTICDAYNVVAHDPPSPFHKSLDTIRKEMWETKTDHSLYVAPVIGTVSSF 60
Db 1 MNNVLNNGRTTICDAYNVVAHDPPSPFHKSLDTIRKEMWETKTDHSLYVAPVIGTVSSF 60
Qy 61 LLKKVSLGKRLISELWGLIFPSGSTNLMDILRETEQFLNQLNLTDLARVNAEGL 120
Db 61 LLKKVSLGKRLISELWGLIFPSGSTNLMDILRETEQFLNQLNLTDLARVNAEGL 120
Qy 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMOQLFLNRLPQFQIQYQLLLPLFAQA 180
Db 121 QANIREFNQVDNLFNPTQNPVPLSITSSVNTMOQLFLNRLPQFQIQYQLLLPLFAQA 180
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Db 69 KILGTGVPFAGQVASYL-SFILGELM-----PKGK-NQWEIFMEHVEEIIINQKISTYARN 122
Qy 112 RVNAELGLOANIREFNOQVDNFPNTPONVPLSIT-SSVNTMQOLFNLRLPQFRVQGYQ 170
Db 123 KALTDLKGLDALAVYHDSLESVGNRNTRARSVKSQVIALBLMFVKQLPSPFVSGEE 182
Qy 171 LLLPLFAQAAWHLSIRDVVLNADWGIISATLRYQNYLKNYTYEYNYCINTYQTA 230
Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSDHCVKYSTG 242
Qy 231 FRGL-NTRLHDM-----EFRTYMLNVEYVSIWLSFKYQSLVSSGANL-----YASGSGP 282
Db 243 LNNLRGNAESWRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLREVYTDAGT 302
Qy 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-VYLVGFSG 313
Db 303 VHPHPSFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMWGG 362
Qy 314 ARLTQTPNIGGLPGTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLTPFV 373
Db 363 HKL--EFRTIGGLNIST-----QGSTNTSINPVLTPFT 394
Qy 374 RSWLDSGSDRGVNTV-----NWQ--TESFESTLGLRCGAFARGNSYFPD 419
Db 395 SRDVRTESLAGLNLFLTHPVGVRVDFHVKFVTHPIAS-----DNFYPG 441
Qy 420 YFIRNISGVPLVARNEDLRPLHYNEIRNIESPGTGGRLAYMVSVHNRKNIIYA-VHE 478
Db 442 Y-----AGIGTQDSENELPPEATGQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494
Qy 479 NGTMHLAPEDYTGFTISPIHATQV-----NNQTRTFISEKFG-NOGDSLRPEQSNNTA 531
Db 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILR--RTNTGT 543
Qy 532 RYTLRGN-----SYNLYRVSLSGNTIRVTINGRVYTAGSNVNTTNNNGVNDNGARF 586
Db 544 FGDIRVINPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596
Qy 587 LDINMGVNASDNTNVPDLINVT-----FNSGTQFELMNMVPTNL 628
Db 597 LDYKTFRTVGTTPFSLDQSTFTIGAWNFSSGNEVYIDRIEFVPEV 645

RESULT 8

O85796 ID O85796 PRELIMINARY; PRT; 719 AA.
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Insecticidal protein.
GN CRV101.
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RC STRAIN=5101;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.C.
DR InterPro; IPR005638; endotoxin.N.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match

9.8%; Score 325.5; DB 2; Length 719;

Best Local Similarity 22.7%; Pred. No. 1.6e-13;
Matches 161; Conservative 103; Mismatches 272; Indels 173; Gaps 32;
Qy 21 HOPFSPEHK-----SLDTIRKEW-MEWKRTDH-----SLY--VAP----- 52
Db 9 HQSFSSNAKVDKISTDSLKNETDIELONINHEHCLKMSVENVEFPVSASTIOTGIGIAG 68
Qy 53 -IVGTSSFLKKVGLIGKRIKSELWGLIFPSGSTNLMDILRETEQPLNORLNTDTLA 111
Db 69 KILGTGVPFAGQVASYL-SFILGELW-----PKGK-NQWEIFMEHVEEIIINQKISTYARN 122
Qy 112 RVNAELGLOANIREFNOQVDNFPNTPONVPLSIT-SSVNTMQOLFNLRLPQFRVQGYQ 170
Db 123 KALTDLKGLDALAVYHDSLESVGNRNTRARSVKSQVIALBLMFVKQLPSPFVSGEE 182
Qy 171 LLLPLFAQAAWHLSIRDVVLNADWGIISATLRYQNYLKNYTYEYNYCINTYQTA 230
Db 183 VPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYSDHCVKYSTG 242
Qy 231 FRGL-NTRLHDM-----EFRTYMLNVEYVSIWLSFKYQSLVSSGANL-----YASGSGP 282
Db 243 LNNLRGNAESWRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLREVYTDAGT 302
Qy 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-VYLVGFSG 313
Db 303 VHPHPSFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMMWGG 362
Qy 314 ARLTQTPNIGGLPGTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLTPFV 373
Db 363 HKL--EFRTIGGLNIST-----QGSTNTSINPVLTPFT 394
Qy 374 RSWLDSGSDRGVNTV-----NWQ--TESFESTLGLRCGAFARGNSYFPD 419
Db 395 SRDVRTESLAGLNLFLTHPVGVRVDFHVKFVTHPIAS-----DNFYPG 441
Qy 420 YFIRNISGVPLVARNEDLRPLHYNEIRNIESPGTGGRLAYMVSVHNRKNIIYA-VHE 478
Db 442 Y-----AGIGTQDSENELPPEATGQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494
Qy 479 NGTMHLAPEDYTGFTISPIHATQV-----NNQTRTFISEKFG-NOGDSLRPEQSNNTA 531
Db 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILR--RTNTGT 543
Qy 532 RYTLRGN-----GNSYNLYRVSLSGNTIRVTINGRVYTAGSNVNTTNNNGVNDNGARF 586
Db 544 FGDIRVINPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596
Qy 587 LDINMGVNASDNTNVPDLINVT-----FNSGTQFELMNMVPTNL 628
Db 597 LDYKTFRTVGTTPFSLDQSTFTIGAWNFSSGNEVYIDRIEFVPEV 645

RESULT 9
O8K161 ID O8K161 PRELIMINARY; PRT; 719 AA.
AC O8K161;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cry.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RC SEQUENCE FROM N.A.
RA Porcar M., Martinez C., Caballero P.;
RL "Identification and characterization of a novel cry gene from Bacillus thuringiensis".
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF278797; AAM73516.1; -.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.

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DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 719 AA; 80964 MW; 84F1287246264473 CRC64;

Query Match          9.8%; Score 323.5; DB 2; Length 719;
Best Local Similarity 22.7%; Pred. No. 2.1e-13;
Matches 160; Conservative 111; Mismatches 269; Indels 165; Gaps 34;

Qy 21 HDPSPFHK-----SLDIRKEM-NEWKRDH-----SLY--VAP-----52
Dy 9 HQSFSSNAKVDKIDTSLSKNETDIELQINHEDECLKISEYENVPFVSASTIQTGISIAG 68
Qy 53 -IVGTVSFLLKKVGLIGKILSELGLIPSPGSTNLMDILRETEQFLNRLNTDTLA 111
Dy 69 KILGTGVPPFAGQVASLY-SFILGELW-----PKGK-NQWEIFMEHVEEIIINQKISTYARN 122
Qy 112 RVNAELGLEQANIREFNQVDNFINPTQNPVPLSIT--SSVNTMQQLFLNRLPQFRVQGYQ 170
Dy 123 KALTDLKGGLDALAVYHESLESWGKRNKTRARSVKVKSQVIALELMFVQKLPFAVSSEE 182
Qy 171 LLLPLPFAQANMHLSPIRDVLNADENGISAATLRTYQNYLKNYTYTEYNICYNTQTA 230
Dy 183 VPLLPIVAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTG 242
Qy 231 FRGL-NTRLHMDL---EFRTYMLNVEYYSIWSLFKYQSLL--VSSGANL-----YASGS 280
Dy 243 LNNLRGNASWRYNFRKDMTLMVLQVALFP--SYDTLVPIKITSQLTREVYTDAL 300
Qy 281 GP-QQTSFTSQDW-----PFL-----YSLFQVNSN-YVLNGF 311
Dy 301 GTVHPNASFASTWYNNNAPSFSIESAVVNPVPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
Qy 312 SGARLTQTFNIGLPGTTTHALLAARVNVGSGDGAIVNQNFSCSTFLPPLLT 371
Dy 361 GGHL--EFRTIGMLNTST-----QGSTNTSINPVTL 392
Qy 372 FVRSWLDGSDRGGVNTVT-----NMQ--TESFESTLGLRCGAFARGNSNYF 417
Dy 393 FTSRDVTRTESLAGLNLFLQPVNGVPRVDFHMKVTHPIAS-----DNFY 439
Qy 418 PDYFIRNISGVPLVVRNEDLRPLHYNEIRNIESPGTGGRLAYMVSVHNRKNNIYA-V 476
Dy 440 PGY-----AGIGTQDSENELPETTGQPNYESYSHRLSHIG--LISASHVKALVYSWT 492
Qy 477 HENGTMIHLAPEDYTGTTISPIHATQV-----NNQTRTFISEKFG-NQGDLSRFEOSNT 529
Dy 493 HRSA-----DRTN-TIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILR--RTNT 541
Qy 530 TARYTLRNGN-----SYNLYLRVSSLGNSITRTVINGRYVYASNVNTTNNQVNDNGA 584
Dy 542 GTFGDIRNINPPAQRVIRVASTTDIQHTSINKKAINQGNFSATMNR-GEGLDYK 600
Qy 585 RFLDINNMGVNASDNTNVPDINV-TFNSGTQFELMIMFVPTNL 628
Dy 601 TFRVGTTFPSFSDVOSTTIGAWNFSNGEVVIDRIEFVPEV 645

RESULT 10
Qy Q9F0P8 PRELIMINARY; PRT; 719 AA.
ID Q9F0P8
AC Q9F0P8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Crv11.
DE Crv11.
GN Crv11.
OS Bacillus thuringiensis.
OG Plasmid pBFC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=BTC007;
RA Song F., Zhang J., Huang D., Li G.;
RT "The cloning of a novel cryII gene from Bacillus thuringiensis
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF211190; AAG43526.1; -.
DR HSP; P02965; 1CIV.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Plasmid.
SQ SEQUENCE 719 AA; 81025 MW; 7E17481922C435E6 CRC64;

Query Match          9.6%; Score 317.5; DB 2; Length 719;
Best Local Similarity 22.7%; Pred. No. 5.4e-13;
Matches 154; Conservative 113; Mismatches 273; Indels 139; Gaps 32;

Qy 19 VAHDPP--SFEHKSLLDIRKEMWKRKTDHSLYVA-PIVGTVSFLLKKVGLIGKRLS 75
Dy 37 INHEDFLRSEHSID----PFVSASTIQTGIGIAGKILGTGVPPFAGQIASLY-SFIL 91
Qy 76 ELWGLIFPSGSTNLMDILRETEQFLNRLNTDTLARVNAELGLEQANIREFNQVDN 135
Dy 92 ELW-----PKGKQ--WEIFMEHVEELIDQKISTYARNIALADLKGDLALAVYHES 146
Qy 136 NPTQNPVPLSIT--SSVNTMQQLFLNRLPQFRVQGYQLLLPLFAQANMHLSPIRD 194
Dy 147 KRNRRARATSVKVSQVIALELLFVQKLPFAVSSEEVPPLPIVAQANLHLLLRDAS 206
Qy 195 ADEWGLISAATLRTYQNYLKNYTYTEYNICYNTQTAFRGL-NTRLHMDL---EFRT 250
Dy 207 GREWGLNSQISTFYNRQVERTSYSDHCVKWYSTGLNLRGNASWRYNFRKDMT 266
Qy 251 NYPEVYSIWSLFKYQSLL--VSSGANL-----YASGSGP-QQTSFTSQDW----- 293
Dy 267 MULDIALFP--SYDTLVPIKITSQLTREVYTDALGTVHPNASFASTWYNNNAPS 324
Qy 294 -----PFL-----YSLFQVNSN-YVLNGFSGARLTQTFNIGLPGTTTHAL 335
Dy 325 IESAVVNPVPHLLDFLEQVTIYSLSRWSNTQYNNMWGGHRL--EFRTIGVLTNTST- 378
Qy 336 LAARVNVGSGSGDGAIVNQNFSCSTFLPPLLTFFVRSWLDGSDRGGVNTVT----- 390
Dy 379 -----QGSTNTSINPVTLPTSRDVTYTESLAGLNLFLQPVN 416
Qy 391 -----NMQTESFESTLGLRCGAFARGNSNYFDPYFIRNISGVPLVVRNEDLRPL 443
Dy 417 GVPRVDFHMKF-----ATLPIASDNF-----YLYG-----AGVTQDSENELP 460
Qy 444 NEIRNIESPGTGGRLAYMVSVHNRKNNIYA-VHENGTMHILAPEDYTGTTISPIHAT 502
Dy 461 TQGPVYESYSHRLSHIG--LISASHVKALVYSWTHSA-----DRTN-TIEPNSIT 509
Qy 503 V-----NNQTRTFISEKFG-NQGDLSRFEOSNTTARYTLRNGN-----SYNLY 550
Dy 510 IPLVKAFLNLSGAAVVRGPGFTGGDILR--RTNTGTFGDIRNINPPAQRVIRV 567
Qy 551 LGNSTIRVTINGRYVYASNVNTTNNQVNDNGARFLDINNMGVNASDNTNVPDINV-T 609
Dy 568 TTDLQHTSINKKAINQGNFSATMNR-GEGLDYKTFRTVGTTFPSFSDVOSTTIGAWN 626
Qy 610 FNSGTQFELMIMFVPTNL 628
Dy 627 FSSGNEVIDRIEFVPEV 645

RESULT 11
Q9SSV8
ID Q9SSV8
AC Q9SSV8;
PRT; 1180 AA.
PRELIMINARY;
```

DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE BT84A1 crystal protein (Crystal protein CryIA).
GN BT84A1.
OS Bacillus thuringiensis, and
OS Bacillus thuringiensis (subsp. sotto).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428, 29340;
RN [1]
RP SPECIES=FROM N.A.
RC SPECIES=B.thuringiensis; STRAIN=T84A1;
RA Nagamatsu Y.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC SPECIES=B.thuringiensis; STRAIN=T84A1;
RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
RT "Nucleotide Sequence of the Lepidoptera-toxic Protein Gene of Bacillus
RT thuringiensis subsp. dendrolimus T84A1.";
RL J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
RN [3]
RN SEQUENCE FROM N.A.
RC SPECIES=B.thuringiensis; STRAIN=T84A1;
RA Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
RT "A Toxic Fragment from the Entomocidal Crystall Protein of Bacillus
RT thuringiensis.";
RL Agric. Biol. Chem. 48:611-619(1984).
RN [4]
RN SEQUENCE FROM N.A.
RC SPECIES=B.thuringiensis (subsp. sotto);
RA Zhong W.F., Cai P.Z., Yan W.Z., Zhang X.X., Xiang Y.W.;
RT "A cryIA gene cloned from Bacillus thuringiensis serovar sotto.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026261; BAA77213.1; -
DR EMBL; AF510713; AAM44305.1; -
DR HSSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin_1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 1180 AA; 133489 MW; 1199EA6D1DC862D CRC64;

Query Match 8.5%; Score 280.5; DB 2; Length 1180;
Best Local Similarity 21.7%; Pred. No. 3.4e-10;
Matches 152; Conservative 104; Mismatches 272; Indels 173; Gaps 29;

Qy 6 NNGRTTCDAYNVVAHDPFSEHKSLDTRKEMWEMKRT--DHSLYVAPIVGTVSSFLK 63
Db 3 NNPNINECIPYNCLS-----NPEVEVLGGERIETGVTIDISL-----SLTQFLLS 48

Qy 64 K----VCSLTKRILSELWGLIFPSGSGTNLMQDILRETEQFLNQLRNLDTLAVNVBLEG 119
Db 49 EFVEGAGFVLG--LVDDIINGIFGS-----QWDAFLVQIEQLINQRIEFARNQAISLEG 102

Qy 120 LQ-----ANIREFNQVDNFLTQNPVLSITSSVNTMQFLNRLPQFVQYQLL 172
Db 103 LSNLYQIYASFRWE-----ADTPALKEEMRIQFNDMNSALTTAIFLAVQNTQVP 156

Qy 173 LPLFAQAANHLSPFRDVLNADWGISAATLRYQNLKYNITYTESNYCINTYQAFR 232
Db 157 LLSVYVQAANHLSLRDVSVFGWGFDAATINSRYNDLTRLIGNYTDYAVRYNTGLE 216

Qy 233 ---GLNTRLHMDL---EFRTYMFNLNVEYVSIWLFKYSLLVSSGANLVASGGPQQTQ 286
Db 217 RVWGPDSR--DWVRYNQFRRELTITLVDIVALFS-----NYDSRRYPIRTV 260

Qy 287 SFTSODPFYLSLQVNSVYLVNGFSGA-----RLTQTF--PNIGGLPGTTTTHALLAA 338
Db 261 SOLTR-----EYTNPNVLENFDGSRGMAQRIEQNTRQPHMLDILNRTIYTDVHR 311

Qy 339 RVNYSOG--VSSGDICAVFNQNFSCSTF-----LPPLLTLP----- 371
Db 312 GFNYMSGHQITASPVG-----FSGPEFAPPLFGNAGNAAPPVLSLTGLGIFRTLSPL 365

Qy 372 FVRSWLDGSDRGVNTVNTWOTESPESTLGRCGAFTARGNSYFPDPYFIRNISGVPLV 431
Db 366 YRRIILGSGPNQELFVLGTEFSPASLTNLPSTIYRQGT-----VSDLDVIPPQ 417

Qy 432 VRNEDLRRLPHY--NEIRNIESPSGTPGGLRAYMVSVHNRK---NNIYAVHE----- 478
Db 418 DNSVPPRAGFSHRLSHVTMLSOAAGAVYTLRAPTFSWQHSRAEFNNIIPSSQITQIPLTK 477

Qy 479 -----NCTMIHLAPEDYTGFTTSPHATQVNNQTRTFISEKFGNCGDSLRFESQNTARY 533
Db 478 STNLGSGTSVVRGP-----GFT-----GGDILR--RTSPQGIS 508

Qy 534 TLGRN-----GNSYNYLVRVSLGNSITRVITNGRVYTTASNVNTTNNQVNDNGARFLD 598
Db 509 TLAVNTAPLSQRYRYRIYASTTNLQFHTSIDGRPINQGNFSATMSS--GSNLOSQSPRT 567

Qy 589 INMGNVVASDNTNVLPLINV--TFNSGTQFELMNMIFVPTNL 628
Db 568 VGTPTPFNFSGSVPTLSARHVNSGNEVVIDRIEVPVPAEV 608

RESULT 12
Q9S603 PRELIMINARY; PRT; 645 AA.
ID AC Q9S603;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Delta-endotoxin (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=serovar japonensis type;
RX MEDLINE=99025985; PubMed=9806979;
RA Wasano N., Ohba M.;
RT "Assignment of delta-endotoxin genes of the four lepidoptera-specific
RT Bacillus thuringiensis strains that produce spherical parasporal
RT inclusions.";
RL Curr. Microbiol. 37:408-411(1998).
DR EMBL; AF042733; AAB97923.1; -
DR HSSP; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin_1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
FT NON_TER 1 1
FT NON_TER 645 645
SQ SEQUENCE 645 AA; 72967 MW; 143B51312B890CE3 CRC64;

Query Match 8.4%; Score 279.5; DB 2; Length 645;
Best Local Similarity 22.1%; Pred. No. 1.7e-10;
Matches 149; Conservative 94; Mismatches 276; Indels 155; Gaps 28;

Qy 13 CDAYNVVAHDPFSEHKSLDTRKEMWEMKRTDHSLYVAPIVG---TVSFLKLVGSLI 69
Db 4 CPADDVVKYPLTDPPNAGLQNM--NYKEYLQTYGGDYTDPLINPLSVSGKDVQVGINI 61

Qy 70 GKRLS-----ELWGLIFPSGSGTNLMQDILRETEQFLNQLRNLDTLAVNV 114
Db 62 VGRLLSFFGFPSSQWTVYTYLLNSLWPDENSVDADFMRVEELIDOKISEAVKGRAL 121

Qy 115 AELEGLOANIREFNQVDNFLTQNPVLSITSSVNTMQFLNRLPQF---RVQGYO 170
Db 122 DDUTGLQYNLYVEALDEWLNRPNGARSLVSRFNILDSLTQFMPSPGSGQNYA 181

```

QY 171 LLLPLFAQANMHLSPFRDVLNADWEGISAAATRTYQNYLKNYKNTTEYSNYCINTYOTA 230
D 172 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 173 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 174 VPLMVAQAANLHLLLDASLFGSEFGLTSOIQYIYERQVERTRDYSYCVWNTG 233
D 175 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 230 --AFRGLN---TRLHMLFRTYMFNLNVEYYSIMSLFKYQSLVSSGANL---YASG 279
D 231 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 232 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 233 LNSLRGTNAASWRYN---QFRDLTLGVLDLVALPSPYDTRTPYINTSAQLTREVYTD 290
D 234 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 280 SGPOQTQSFTSQDW-----PFL-----YSLFQVNSNYV-----LNGF 311
D 281 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 291 IGATGV-NMASNMWYNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTY 349
QY 312 SGARLTOTPNIGGLPGCTTTTHALLAARVN-----YSGVSSGDCGAVF 355
D 313 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 350 RG-RTIQSRPIGGGL---NTSTHGTNTSINPVTLPFASRDVYRTESYAGVLLWG----- 400
QY 356 NONFSCSTELPPLLTTPFVRSWLDGSDRGVNTV---TNWQTESPESTLGLRCGAFAR 411
D 357 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 401 -----IYLEPI-----HGVPTVRFNFTNPQN-----ISDR 425
QY 412 GMSNYPPDYFIRNISGVPLVWRNEDLRRLPHYNEIRNIESPSGTPGGLRAYMVSVNRKN 471
D 413 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 426 GTANYSQPY-----ESPGQLKDSLETLPETTERPNYESYSHR---LSHIGILQSRVN 477
QY 472 -NIYA-VHENGTMHILAPEDYTGFTTSPHATQVNNQTRTFISEKEFGNQDSLRFPQSNT 529
D 473 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 478 VPYISWTHRSA-----DRTN-TIGPNRITQI-----PMVKASELPQGTTV----- 516
QY 530 TARYTLRGNG-NSYNLRLVSSLSGNSITRVING-----RVYTASNVTNTNNDG 578
D 531 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 517 -----VRGFGTGGDILRLTNTGCGFPIRVNNGPLTQYRIGFRVASTVDPFFVSRGG 571
QY 579 VNDNGARFL-----DINMGVNV-----ASDNTNVPDLD--- 605
D 572 TTVNFRFLRTMNSGDELKYGFRRAFTTPFTTQIQDIIRTSIQGLSGNGEVYIDKIE 631
QY 606 -INVTFNSGTQFEL-----MNIMFVPTN 627
D 632 IIPVTATFEAYDLERAQEAVALFTNTN 660

```

RESULT 14

Q45740

ID Q45740 PRELIMINARY; PRT; 381 AA.

AC Q45740;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Insecticidal crystal protein (CryIF) (Fragment).

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EG6346;

RX MEDLINE=91286178; PubMed=2061280;

RA Chambers J.A., Jelen A., Gilbert M.P., Jany C.S., Johnson T.B.,

RA Gawton-Burke C.;

RT "Isolation and characterization of a novel insecticidal crystal

RT protein gene from Bacillus thuringiensis subsp. aizawai.";

RL J. Bacteriol. 173:3966-3976 (1991).

DR EMBL; M63897; AAA2349.1; -.

DR HSSP; P071130; 1DLIC.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF00555; endotoxin; 1.

DR Pfam; PF03945; endotoxin_N; 1.

FT NON_TER 381

SQ SEQUENCE 381 AA; 42967 MW; DDAEF0D0504CE96C CRC64;

Query Match

8.4%; Score 277.5; DB 2; Length 381;

Best Local Similarity 26.3%; Pred. No. 1.1e-10;

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QY 171 LLLPLFAQANMHLSPFRDVLNADWEGISAAATRTYQNYLKNYKNTTEYSNYCINTYOTA 230
D 172 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 173 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 174 VPLMVAQAANLHLLLDASLFGSEFGLTSOIQYIYERQVERTRDYSYCVWNTG 233
D 175 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 230 --AFRGLN---TRLHMLFRTYMFNLNVEYYSIMSLFKYQSLVSSGANL---YASG 279
D 231 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 232 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 233 LNSLRGTNAASWRYN---QFRDLTLGVLDLVALPSPYDTRTPYINTSAQLTREVYTD 290
D 234 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 280 SGPOQTQSFTSQDW-----PFL-----YSLFQVNSNYV-----LNGF 311
D 281 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 291 IGATGV-NMASNMWYNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSASSRWSNTRHMTY 349
QY 312 SGARLTOTPNIGGLPGCTTTTHALLAARVN-----YSGVSSGDCGAVF 355
D 313 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 350 RG-RTIQSRPIGGGL---NTSTHGTNTSINPVTLPFASRDVYRTESYAGVLLWG----- 400
QY 356 NONFSCSTELPPLLTTPFVRSWLDGSDRGVNTV---TNWQTESPESTLGLRCGAFAR 411
D 357 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 401 -----IYLEPI-----HGVPTVRFNFTNPQN-----ISDR 425
QY 412 GMSNYPPDYFIRNISGVPLVWRNEDLRRLPHYNEIRNIESPSGTPGGLRAYMVSVNRKN 471
D 413 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 426 GTANYSQPY-----ESPGQLKDSLETLPETTERPNYESYSHR---LSHIGILQSRVN 477
QY 472 -NIYA-VHENGTMHILAPEDYTGFTTSPHATQVNNQTRTFISEKEFGNQDSLRFPQSNT 529
D 473 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 478 VPYISWTHRSA-----DRTN-TIGPNRITQI-----PMVKASELPQGTTV----- 516
QY 530 TARYTLRGNG-NSYNLRLVSSLSGNSITRVING-----RVYTASNVTNTNNDG 578
D 531 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 517 -----VRGFGTGGDILRLTNTGCGFPIRVNNGPLTQYRIGFRVASTVDPFFVSRGG 571
QY 579 VNDNGARFL-----DINMGVNV-----ASDNTNVPDLD--- 605
D 572 TTVNFRFLRTMNSGDELKYGFRRAFTTPFTTQIQDIIRTSIQGLSGNGEVYIDKIE 631
QY 606 -INVTFNSGTQFEL-----MNIMFVPTN 627
D 632 IIPVTATFEAYDLERAQEAVALFTNTN 660

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RESULT 13

Q93NM5

ID Q93NM5 PRELIMINARY; PRT; 1228 AA.

AC Q93NM5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE CryIa.

GN CryIa.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang J., Song F., Huang D.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF368257; AAK63251.1; -.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_C.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF00555; endotoxin; 1.

DR Pfam; PF03944; endotoxin_C; 1.

DR Pfam; PF03945; endotoxin_N; 1.

SQ SEQUENCE 1228 AA; 139666 MW; E86D9842341PB439 CRC64;

Query Match

8.4%; Score 278.5; DB 2; Length 1228;

Best Local Similarity 22.1%; Pred. No. 4.8e-10;

Matches 152; Conservative 100; Mismatches 228; Indels 209; Gaps 33;

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QY 52 PIVGTSSFLKKVGLSGILKRLSLMGLIFPSGSTNLMODILRETEQFLNORLNTDTLA 111
D 53 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 68 PFAGQLASFYSFLVG-----ELW-----PRG-RDWEIFLEHVEQLINQITENARN 113
QY 112 RVNAELGLOANIREFNQVDNFINPQNVPVLSITSSVNTMOQL-FLNRLPQFRVQGYQ 170
D 113 :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 114 TALARLQGLGDSFRAYQOSLEDWLENRDDARTSRVLYTVIALELDFLNAMPLFAIRNOE 173

```

Matches 100; Conservative 66; Mismatches 135; Indels 79; Gaps 19;

QY 21 HDPSFPHK-----SLDTIRKEM-MEWKRTDH-----SLY--VAP-----52

Db 9 HQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKISEYENVEPFSASTIQTGISIAG 68

QY 53 -IVGTSSFLKKVGLIGKRIILSELWGLFPSPGSTNLMQDILRETEQFLNQRINTDTLA 111

Db 69 KILGTGVPAGQVASLY-SFILGELW-----PKGK-NQWEIFMEHVEEIIINQISTYARN 122

QY 112 RVNAELEGQANIREFNQVDNPLNPTQNPVLSIT--SSVNTMQQLFLNRLPQFRVQGYQ 170

Db 123 KALTDLKGGLDALAVHESLESWGNERKNTPARSVKVSQVIALELMFVQKLPSFASGEE 182

QY 171 LLLPLFAQAANMHLSTFIRVDVNLADWGIISAATLRTYQNYLKNYTYEYSNICYNTYQTA 230

Db 183 VPLLPYIAQAANLHLLLRDASIFGKWLSSSEISFTYRQVERAGDYSCHVKWYSTG 242

QY 231 FRGL-NTRLHML---EFRTYMLNVEYVINSFLKYSQSL--VSGANL-----YASGS 280

Db 243 LNNLRGTNAESWRYNQFRKDMTLMVLDLVALFP--SYDTLVYPIKTSQLTREVYTDAL 300

QY 281 GP-QOTQSFTSQDW-----PFL-----YSLFQVNSN-VYLNCF 311

Db 301 GTVHPNASFASTWYNNAPSFSTIESAVVRNPHLLDFLEQVTIYSLLSRWSTQTNMWM 360

QY 312 SGARLTQTFNIGLPGTTTT 331

Db 361 GGHRL--EFRTIGGLMTST 378

RESULT 15

Q45720 PRELIMINARY; PRT; 620 AA.

AC Q45720;

DT 01-NOV-1996 (TEMBLrel. 01, Created)

DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)

DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)

DE CryIA(a) (Fragment).

GN CRYIA(A).

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NRD-12;

RX MEDLINE=95386467; PubMed=7657602;

RA Masson L., Lu Y.J., Mazza A., Brousseau R., Adang M.J.;

RT "The CryIA(c) receptor purified from Manduca sexta displays multiple

RL specificities."

RL J. Biol. Chem. 270:20309-20315(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=NRD-12;

RX MEDLINE=95231292; PubMed=7715447;

RA Masson L., Mazza A., Gringorten L., Baines D., Aneliunas V.,

RA Brousseau R.;

RT "Specificity domain localization of Bacillus thuringiensis

RL insecticidal toxins is highly dependent on the bioassay system."

RL Mol. Microbiol. 14:851-860(1994).

DR EMBL; U43605; AAA86265.1; -.

DR HSSP; P02965; 1CIY.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_C.

DR InterPro; IPR005639; endotoxin_N.

DR Pfam; PF00555; endotoxin; 1.

DR Pfam; PF03944; endotoxin_C; 1.

DR Pfam; PF03945; endotoxin_N; 1.

FT NON_TER 1

FT NON_TER 620

SQ SEQUENCE 620 AA; 69428 MW; 4571A09B5656EDE CRC64;

Query Match

8.3%; Score 276.5; DB 2; Length 620;

Best Local Similarity 21.5%; Pred. No. 2.5e-10;

Matches 151; Conservative 105; Mismatches 272; Indels 173; Gaps 29;

QY 6 NNGRTTICDAYNVVAHDPSFSEHKSLDTIRKEMWKRT--DHSLYVAPITGVSSFLLK 63

Db 3 NNPINECIPYNCL-----NPEVEVLGGRIETGYTPIDISL-----SLTQFLLS 48

QY 64 K-----VSGLIIGKRIILSELWGLFPSPGSTNLMQDILRETEQFLNQRINTDTLARVNALEG 119

Db 49 EFVPGAGFVLG--LVDIIMGIFGPS---QWDAFLVQIEQLINQRIIEEFARNOAISRLG 102

QY 120 LQ-----ANIREFNQVDNPLNPTQNPVLSITSSVNTMQQLFLNRLPQFRVQGYQ 172

Db 103 LSNLYQIYAESPREME-----ADPTNPAIREMRIQFNDMSALTATPLLAQVQV 156

QY 173 LLLPLFAQAANMHLSTFIRVDVNLADWGIISAATLRTYQNYLKNYTYEYSNICYNTYQTA 232

Db 157 LLSVYQAANLHLLSVLRDVSFGQWGFDAATINSRYNDLTRLIGNYTDYAVRYNTGLE 216

QY 233 ---GLNTRLHML---EFRTYMLNVEYVINSFLKYSQSL--VSGANL-----YASGS 286

Db 217 RVMGPDNR--DWRYNQFRRLTLTVLDIVLFS-----NYDSRRYBIRT 260

QY 287 SFTSQDWPLYSLFQVNSYVNLGFSGA-----RLTQTF--PNIGGLPGTTTHALLAA 338

Db 261 SOLTR-----EYITNPVLENFDGSPRMAQRIEQNIQPHLMDILNSITITVDVHR 311

QY 339 RVNYSGG--VSSGDIGAVFNQFSCSTF-----LPPLLT----- 371

Db 312 GFNYSGHQITASPVG-----FSGPEFAFPFGNAGNAAPPVLVSLTGLGIPRTLSPL 365

QY 372 FVRSWLDGSGDRGVNTVTNMQTESFESTLGRCGAFTARGNSNYPPDYFIRNIGVPLV 431

Db 366 YRRILGSGPNQELFVLGTFSPASLTNLPSTIYRQGT-----VDSLVDVIPPQ 417

QY 432 VRNEDLRRLPHY--NEIRNIESPGTGPCGLRAYMVSVHNRK---NNIYAVHE----- 478

Db 418 DNSVPPRAGFSHRLSHVTLVLSQAAGAVYTLRAPTFWQHRSAEFNNIIPSSQITQIPLT 477

QY 479 ----NGTWIHLAPEDYTGTTISPIHATQVNNQTRTFISEKFGNQDGLRFEQSNTTARY 533

Db 478 STNLSGTSVVKGP---GFT-----GGDIIR--RTSPGQIS 508

QY 534 TLRLGN-----GNSYNYLVRVSSLGNSTIRVTINGRVYITASNVNNTTNDGVNDNGARPLD 588

Db 509 TLRVNTITAPLSQRYRVRIRYASTTNLQPHTSIDGRPINQGNFSATWSS--GSNLQSGSPRT 567

QY 589 INMGNVVASDNTNVPIDINV--TFNSGTQFELNMIMFVPTNL 628

Db 568 VGFPTTPNFNSGSSVFTLSAHVFNSEGVYIDRIEFVPAEV 608

Search completed: December 12, 2003, 16:17:37

Job time : 42 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 16:10:35 ; Search time 17 Seconds
(without alignments)
1748.287 Million cell updates/sec

Title: US-10-040-906A-2
Perfect score: 3314
Sequence: 1 MNVNLNNGRTTICDAYNVA.....GTQFELNMFVPTNLPPIY 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3048.5	92.0	633	1 C2AA_BACTK	P21253 bacillus th
2	3030.5	90.8	633	1 C2AB_BACTK	P21254 bacillus th
3	2916.5	88.0	633	1 C2AC_BACTU	Q9rmg3 bacillus th
4	2545	76.8	622	1 C2AD_BACTU	Q45743 bacillus th
5	1087	32.6	675	1 C1BA_PABPP	P57091 paenibacill
6	1080	32.6	705	1 C1AA_PABPP	Q45358 paenibacill
7	1073.5	32.4	695	1 C1CA_PABPP	P57092 paenibacill
8	336.5	10.2	643	1 C2AA_BACTI	P21256 bacillus th
9	327.5	9.9	719	1 C1IA_BACTK	Q45752 bacillus th
10	327.5	9.9	1231	1 C1BD_BACTZ	Q9az25 bacillus th
11	325	9.8	719	1 C1ID_BACTU	Q9xdl1 bacillus th
12	310.5	9.4	719	1 C1IB_BACTE	Q45709 bacillus th
13	307	9.3	1157	1 C1CA_BACTO	Q45733 bacillus th
14	306	9.2	1138	1 C7AB_BACUA	Q45707 bacillus th
15	305.5	9.2	1227	1 C1BE_BACTU	Q85805 bacillus th
16	304.5	9.2	750	1 CBBB_BACTV	Q9zius bacillus th
17	300.5	9.1	682	1 C3BA_BACUH	Q86170 bacillus th
18	294.5	8.9	1176	1 C1CB_BACTG	P56953 bacillus th
19	293.5	8.9	1229	1 C1BB_BACTU	Q45739 bacillus th
20	293.5	8.9	1233	1 C1BC_BACTM	Q45774 bacillus th
21	291.5	8.8	1179	1 C1AD_BACTA	Q30744 bacillus th
22	288.5	8.7	1138	1 C7AB_BACUK	Q45708 bacillus th
23	287	8.7	724	1 C8BA_BACTJ	Q45730 bacillus th
24	283.5	8.5	1169	1 C8BA_BACUK	Q45705 bacillus th
25	280	8.4	1169	1 C3DA_BACTP	Q6014 bacillus th
26	277	8.4	1181	1 C1AE_BACTL	Q30748 bacillus th
27	275.5	8.3	1170	1 C1JB_BACTU	Q45716 bacillus th
28	275.5	8.3	1228	1 C1BA_BACTK	P05517 bacillus th
29	273	8.2	1215	1 C1KA_BACTM	Q45715 bacillus th
30	272.5	8.2	826	1 C3AA_BACUH	Q85597 bacillus th
31	271.5	8.2	1176	1 C1AA_BACUH	P02965 bacillus th
32	270.5	8.2	1174	1 C1EB_BACTA	Q30745 bacillus th
33	268	8.1	1155	1 C1AB_BACTK	P06578 bacillus th

RESULT 1
C2AA_BACTK STANDARD; PRT; 633 AA.
ID P21253; O52764;
AC 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2Aa (insecticidal delta-endotoxin)
DE CryIIa(a) (Crystalline entomocidal protoxin) (71 kDa crystal protein)
DE (P2 crystal protein) (Mosquito factor)
GN CRY2AA OR CRYIIA(A) OR CRYB1 OR CRYII.
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. kenya)
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 33930;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RX MEDLINE=89123178; PubMed=2914879;
RA Widner W.R., Whiteley H.R.;
RT "Two highly related insecticidal crystal proteins of Bacillus
thuringiensis subsp. kurstaki possess different host range
specificities."
RL J. Bacteriol. 171:965-974 (1989).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.
RC SPECIES=B.t.kurstaki; STRAIN=HD-263, and HD-1;
RX MEDLINE=88087146; PubMed=3121615;
RA Donovan W.P., Dankocsk C.C., Gilbert M.P., Gawron-Burke M.C.,
Groat R.G., Carlton B.C.;
RT "Amino acid sequence and entomocidal activity of the P2 crystal
protein. An insect toxin from Bacillus thuringiensis var. kurstaki."
J. Biol. Chem. 263:561-567 (1988).
RN [3]
RP REVISIONS.
RA Donovan W.P., Dankocsk C.C., Gilbert M.P., Gawron-Burke M.C.,
Groat R.G., Carlton B.C.;
RL J. Biol. Chem. 264:4740-4740 (1989).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=4A4C / HD-549;
RA Miera H.S., Khairnar N.P., Mathur M., Donnelly R.J., Mahajan S.K.;
Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES COLLOIDAL LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF BOTH DIPTERAN (AEDES AEGYPTI) AND LEPIDOPTERAN
(MANDUCA SEXTA) LARVAE.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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P05068 bacillus th
Q45738 bacillus th
Q03746 bacillus th
Q45706 bacillus th
Q45748 bacillus th
Q66377 bacillus th
Q9x597 bacillus th
P19415 bacillus th
Q96515 bacillus th
Q45744 bacillus th
Q03749 bacillus th
Q9zn19 bacillus th


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Qy 121 QANIRENQVDNLFNPTQNPVLSITSSVNTMOQLFNLRLPQPRVQGYQLLLPLPAQA 180
Db 121 QANVEENRQVDNLFNPNRAVPLSITSSVNTMOQLFNLRLPQPRVQGYQLLLPLPAQA 180
Qy 181 ANMHLSEIRDVNLNADWEGISAATLRTYQNLKNTTYSNYCINTYTQAFRGLNTRLHD 240
Db 181 ANLHLSFIRDVNLNADWEGISAATLRTYQNLKNTTYSNYCINTYTQAFRGLNTRLHD 240
Qy 241 MLEFRTYMFNLVPEYVSIWLSFKYQSLVSSGANLYASGGPQQTQSTQDWPFLYSLF 300
Db 241 MLEFRTYMFNLVPEYVSIWLSFKYQSLVSSGANLYASGGPQQTQSTQDWPFLYSLF 300
Qy 301 QVNSNYLVNGFSGARLTQTTPNIGGLPGTTTHALLAARVNSYSGVSSGIGA-VFNQNF 359
Db 301 QVNSNYLVNGFSGARLTQTTPNIGGLPGTTTHALLAARVNSYSGVSSGIGA-VFNQNF 360
Qy 360 SCSTFLPPLLTTPFVRSLDSDGSGGVNTVNTWQTESFESTLGLRCAFTARGNSVFPD 419
Db 361 NCSTFLPPLLTTPFVRSLDSDGSGGVNTVNTWQTESFESTLGLRCAFTARGNSVFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 480
Qy 480 GTMIHLAPEDYTGTTSPIHATQVNNQTRTFISEKFGNQGDSLRFESQNTTARYTLRGNG 539
Db 481 GSMIHLAPEDYTGTTSPIHATQVNNQTRTFISEKFGNQGDSLRFESQNTTARYTLRGNG 540
Qy 540 NSYNLYRVSSGLNSTIRVTINGRVYTASVNTTNNNDGVNDNGARFLDINMGVNVASDN 599
Db 541 NSYNLYRVSSGLNSTIRVTINGRVYTASVNTTNNNDGVNDNGARFLDINMGVNVASDN 600
Qy 600 TNVPLDINTVFNSTQGFELMNMIFVPTNLPPIY 632
Db 601 SDVELDINTVFNSTQGFELMNMIFVPTNLPPIY 633

RESULT 3
C2AC_BACTU STANDARD; PRT; 633 AA.
ID C2AC_BACTU AC QRMG3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2ad (Insecticidal delta-endotoxin
DE CryIIA(d) (Crystalline entomocidal protoxin) (71 kDa crystal protein).
GN CRY2AD OR CRYIIA(D) OR CRY2.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.

C2AC_BACTU STANDARD; PRT; 633 AA.
ID C2AC_BACTU AC Q45743;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2ac (Insecticidal delta-endotoxin
DE CryIIA(c) (Crystalline entomocidal protoxin) (70 kDa crystal protein).
GN CRY2AC OR CRYIIA(C) OR CRYIIC.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.

C2AC_BACTU STANDARD; PRT; 622 AA.
ID C2AC_BACTU AC Q45743;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2ac (Insecticidal delta-endotoxin
DE CryIIA(c) (Crystalline entomocidal protoxin) (70 kDa crystal protein).
GN CRY2AC OR CRYIIA(C) OR CRYIIC.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
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DR EMBL; AF200816; AAF09583.1; -.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 633 AA; 70752 MW; 2A582067131B39CB CRC64;

Query Match 88.0%; Score 2916.5; DB 1; Length 633;
Best Local Similarity 87.2%; Pred. No. 2.5e-189;
Matches 552; Conservative 44; Mismatches 36; Indels 1; Gaps 1;

Qy 1 MNVNLNGRITTCADYANVVAHDGFSPEHKSLDTRIRKEWKEWKTDRSLYVAPIVGTVSSP 60
Db 1 MNSVLNNGRITTCADYANVVAHDGFSPEHKSLDTRIRKEWKEWKTDRSLYVAPIVGTVSSP 60
Qy 61 LKAKVGLSLGKRLTSLSELGLIPFSGSTNLMDTLRTEQFLNORLNTDTLARVNAELEG 120
Db 61 LKAKVGLSLGKRLTSLSELGLIPFSGSTNLMDTLRTEQFLNORLNTDTLARVNAELEG 120
Qy 121 QANIRENQVDNLFNPTQNPVLSITSSVNTMOQLFNLRLPQPRVQGYQLLLPLPAQA 180
Db 121 QANVEENRQVDNLFNPNRAVPLSITSSVNTMOQLFNLRLPQPRVQGYQLLLPLPAQA 180
Qy 181 ANMHLSEIRDVNLNADWEGISAATLRTYQNLKNTTYSNYCINTYTQAFRGLNTRLHD 240
Db 181 ANLHLSFIRDVNLNADWEGISAATLRTYQNLKNTTYSNYCINTYTQAFRGLNTRLHD 240
Qy 241 MLEFRTYMFNLVPEYVSIWLSFKYQSLVSSGANLYASGGPQQTQSTQDWPFLYSLF 300
Db 241 MLEFRTYMFNLVPEYVSIWLSFKYQSLVSSGANLYASGGPQQTQSTQDWPFLYSLF 300
Qy 301 QVNSNYLVNGFSGARLTQTTPNIGGLPGTTTHALLAARVNSYSGVSSGDI-GAVFNQNF 359
Db 301 QVNSNYLVNGFSGARLTQTTPNIGGLPGTTTHALLAARVNSYSGVSSGDI-GAVFNQNF 360
Qy 360 SCSTFLPPLLTTPFVRSLDSDGSGGVNTVNTWQTESFESTLGLRCAFTARGNSVFPD 419
Db 361 NCSTFLPPLLTTPFVRSLDSDGSGGVNTVNTWQTESFESTLGLRCAFTARGNSVFPD 420
Qy 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHEN 480
Qy 480 GTMIHLAPEDYTGTTSPIHATQVNNQTRTFISEKFGNQGDSLRFESQNTTARYTLRGNG 539
Db 481 GTMIHLAPEDYTGTTSPIHATQVNNQTRTFISEKFGNQGDSLRFESQNTTARYTLRGNG 540
Qy 540 NSYNLYRVSSGLNSTIRVTINGRVYTASVNTTNNNDGVNDNGARFLDINMGVNVASDN 599
Db 541 NSYNLYRVSSGLNSTIRVTINGRVYTASVNTTNNNDGVNDNGARFLDINMGVNVASDN 600
Qy 600 TNVPLDINTVFNSTQGFELMNMIFVPTNLPPIY 632
Db 601 SDVELDINTVFNSTQGFELMNMIFVPTNLPPIY 633

RESULT 4
C2AC_BACTU STANDARD; PRT; 622 AA.
ID C2AC_BACTU AC Q45743;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry2ac (Insecticidal delta-endotoxin
DE CryIIA(c) (Crystalline entomocidal protoxin) (70 kDa crystal protein).
GN CRY2AC OR CRYIIA(C) OR CRYIIC.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
```

RC STRAIN=Shanghai 1 / S-1;
RX MEDLINE=91340086; PubMed=1651878;
RA Wu D., Cao X.L., Bai Y.Y., Aronson A.I.;
RT "Sequence of an operon containing a novel delta-endotoxin gene from
RL *Bacillus thuringiensis*,"
RL FEMS Microbiol. Lett. 65:31-36(1991).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPIHELIAL CELLS OF LEPIDOPTERAN LARVAE. HAS LOW ACTIVITY ON
CC DIPTERAN LARVAE.
CC
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X57252; CAA40536.1; -.
DR PIR; S17402; S17402.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation; Plasmid.
SQ SEQUENCE 622 AA; 69729 MW; E0B5FAD37BF8299 CRC64;

Query Match 76.8%; Score 2545; DB 1; Length 622;
Best Local Similarity 78.9%; Pred. No. 2.9e-164;
Matches 501; Conservative 45; Mismatches 73; Indels 16; Gaps 8;

QY 1 MNVNLNGRTTCIDAYNVVAHDPFSFEHKSLLDTIRKEMWKRTHSLYVAPIVGTVSSP 60
DB 1 MNTVLNNGRTTCIDAYNVVAHDPFSFEHKSLLDTIRKEMWKRTHSLYVAPIVGTVSSP 60

QY 61 LLKKVGLIGKRLSELWGLIFPFGSGTNLMQDILRETEQFLNQRNLDTLARNVAELEG 120
DB 61 LLKKVGLIGKRLSELWGLIFPFGSGTNLMQDILRETEQFLNQRNLDTLARNVAELEG 120

QY 121 QANIREFNOQVDNFTQNPVPLSITS--SVNTHQQLFLNRLPQFRVGYQLLLPLPAQA 180
DB 121 QANVAEFNRQVDNFTQNPVPLAIDSVNTHQQLFLNRLPQFRVGYQLLLPLPAQA 180

QY 181 ANMHLSTIRDVVNADEWGISAAITRTYQNLKNTTEYSNYCINTYTQAFRGNTLRHD 240
DB 181 ANFNLSTIRGVILNADENGISAAITRTYRDLRKHFRDYSNYCINPYQTAFRGNLRHPD 240

QY 241 MLEFRTYVNLVNFVYVSWLKFQSLVSSGANLYASGGPQQTQSTQSDWPFLYSLF 300
DB 241 MLEFRTYVNLVNFVYVSWLKFQSLVSSGANLYASGGP--TQSTQSDWPFLYSLF 298

QY 301 QVNSNYLVNFGSGARLTQTFPNIQGLP--GTTTHALLAARVYVSGVSGDIDG-AVFNQ 357
DB 299 QVNSNYLVNGLSGARTTTFPNIQGLPVYHNSTLH--FARINRVGGVSSRIGQANLQ 355

QY 358 NFSCSTFLPLLTTPFVRSWLDGSDRGVNTVTWMTQESTIGLCGAFARGNSNYF 417
DB 356 NFNLSTFLPNTQTFPRLSWLDGSDRGVNTVTWMTQESTIGLCGAFARGNSNYF 414

QY 418 PDYFIRNISGVPLVRNEDLRRLHYNEIRNIESPSGTGGLRAYMYSVNHRKNIVAVH 477
DB 415 PDYFIRNISGVVGTISNADLAPLHNEIRDI----GTTA--VASLIVVNRKNIVYDTH 468

QY 478 ENGTMHILAPBDYTGFTISPIHATOVNNQTRTFISEKFGNQDGLRPEQSNNTARYTLRG 537
DB 469 ENGTMHILAPNDYTGFTVSPHATOVNNQTRTFISEKYGQDGLRPELSNPTARYTLRG 528

QY 538 NGNSYNYLVRVSSLSGNSITRTVINGRVYTASNTVNTTNDGVNDNGARFELDINNENNVAS 597
DB 529 NGNSYNYLVRVSSLSGNSITRTVINGRVYTANVTNTTNDGVNDNGARFELDINNENNVAS 587

QY 598 DNTNVPLDINDVFNSTGQFELMNMIFVPTNLPPYI 632
DB 588 ANTNPVLDIQVTFNGNQFELMNMIFVPTNLPPYI 622

RESULT 5
CIBA_PAEPP STANDARD; PRT; 675 AA.
ID CIBA_PAEPP STANDARD; PRT; 675 AA.
AC P57031;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parasporal crystal protein cryIIIBa (Parasporal delta-endotoxin
DE CryXVIIIB(a)) (Crystalline parasporal protoxin) (76 kDa crystal
DE protein).
GN CRY18BA OR CRYXVIIIB(A).
OS *Paenibacillus popilliae* (Bacillus popilliae).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=78057;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP3;
RA Patel R., Yousten A.A., Rippere K.;
RT "Detection of two new cry genes in *Paenibacillus popilliae*,"
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF169250; AAF89667.1; -.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
FT DOMAIN 101 104 POLY-LEU.
FT DOMAIN 199 204 POLY-LEU.
SQ SEQUENCE 675 AA; 75848 MW; 823B58B8A8E81DF5 CRC64;

Query Match 32.8%; Score 1087; DB 1; Length 675;
Best Local Similarity 38.9%; Pred. No. 7.3e-66;
Matches 259; Conservative 104; Mismatches 244; Indels 58; Gaps 19;

QY 2 NVVLNNGRTTCIDAYNVVAHDPFSFEHKSLLDTIRKEMWKRTHSLYVAPIVGTVSSP 60
DB 35 NNIICNGFWPI-----NVRKNP--FRKRTQFIRETEWKENSPSLFTAPIGVVVTST 88

QY 61 LLKKVGLIGKRLSELWGLIFPFGSGTNLMQDILRETEQFLNQRNLDTLARNVAELEG 120
DB 89 LLEALKKQVQSRLLELLMTNLLFPNNSTMTIELRATEQVQVQQLDVTVNRVQSLEGL 148

QY 121 QANIREFNOQVDNFTQNPVPLSITS--SVNTHQQLFLNRLPQFRVGYQLLLPLP 177
DB 149 KNNLRTFNQIDIDFL---QNRVEISPTAMTDSINTWQVFNRLPQFQSLDYQLLLPLP 205

QY 178 AQANMHLSTIRDVVNADEWGISAAITRTYQNLKNTTEYSNYCINTYTQAFRG 234


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114 QCGFPTA-----TAKGFPLNSGAIORLQFQFEVQYEGVSWALFTQMCTLLTLUL 164
189 RDVLNADBWGISAAATLRYQNYLKNYTEYSNICYQTAF-RGLNTRLHDMLEFRY 247
165 KDGIILAGSANGFTQADVDSFKLFNQKVLDRYLRMRMYTEEFGRCLKSVLKDGLTRFN 224
248 MFLNVPEYVWSLFPKYQSLVSSGANLYASGSGPQQTSTQSDWPPFLYSLPQVNSN-- 305
225 CNLYVFPFAEAWSLMYEGLKLQSSLSL-----WDYGVSIPIVNYNEM 267
306 -----YVLNGFSGARLTQFPNIGGLPGTTHHTALLAARVNYSG-----GVSSGDIGAVF 355
268 GGLVYKLLMGENVQRLLTTVKENY---SFTNEPADIPARENIRGVHPIDYDPSSGLTGWIG 323
356 N---ONESCSIFLPPLLTPFVRSWLDSCSGRGVNTVNHQ-----NNGNEIMEVRTQTFYQNPNNPIAPRDIINOILTA 369
324 NORTNENPAD-----NNGNEIMEVRTQTFYQNPNNPIAPRDIINOILTA 369
394 -----TESFESTL---GLRCGGAFTARGN-----SNY--FPDYFIRNI 425
370 PAPADLFFKNADINVKFTQWFQSTLYGNWIKLGTQVLSSRTGTIPPNYLAYDGYIRAI 429
426 SGVPLVVR---NEDLRRLPHVNEIRNTESPG-----TPGGLRAYMVSVHNRKNYIA 475
430 SACPRGVSLAYNHDL-TTLTYNRI-EYDSTPTENIIIVGPAPDNKOF-----YSKKS----- 479
476 VHENGTMIHLAPEDYGTFTSPIHATQVNNOTRTFISEKFGNOCD-SLRPEQO---NTTAR 532
480 -----HYLSETNDSYVIPALQPAEVS-D-RSFLEDTPQATDGSIKFARTFISNEAK 529
533 YTLRGNGSNLYLVRVSSLGNSSTRVINGRVTYASNVNTTNNDGVDNDNGARFLDINNG 592
530 YSIRLNL-TGFNTATRYKLI-----IRVRVPYRL--PAGIRVQSQNSGNN-----RMLGSFTA 578
593 NV-----VASDNTNVPDLINV-TFNSGTQFOLNMIMFV-----PTNL 628
579 NANPEWDEVDTAFDNDLGLTGTSTGNALFISDSDLSNGEEWYLSQLFLVKESAFTQOI 638
629 PPI 631
639 NPL 641

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RESULT 9

CILIA_BACTK	STANDARD;	PRT; 719 AA.
ID CQ45752;	P71092;	Q45750; Q45751; Q45756;
DT 30-MAY-2000	(Rel. 39,	Created)
DT 30-MAY-2000	(Rel. 39,	Last sequence update)
DT 16-OCT-2001	(Rel. 40,	Last annotation update)
DE Pestidical crystal protein cryIIA (Insecticidal delta-endotoxin		
DE CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).		
GN CRYIIA OR CRYII(A) OR CRVY OR CRYVI OR CGCRVY.		
OS Bacillus thuringiensis (subsp. kurstaki).		
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
ON NCBI_TaxID=29339;		
OX [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=DSIR732;		
RX MEDLINE=93298009; PubMed=8517758;		
RA Gleave A.P., Williams R., Hedges R.J.;		
RT "Screening by polymerase chain reaction of Bacillus thuringiensis		
RT serotypes for the presence of cryV-like insecticidal protein genes and		
RT characterization of a cryV gene cloned from B. thuringiensis subsp.		
RT kurstaki";		
RL Appl. Environ. Microbiol. 59:1683-1687(1993).		
LN [2]		
LC SEQUENCE FROM N.A.		
RC STRAIN=JHCC4835;		
RX MEDLINE=92269562; PubMed=1588820;		
RA Tailor R., Tippett J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;		
RT "Identification and characterization of a novel Bacillus thuringiensis		

Db 9 HQSPSSNAKVDKISTDLKNETDIQLQNHEDCLKMEYENVEPVFASTIQTGIGIAG 68
 QY 53 -IVGTSSFLKKGSLGKILSLGLIPSGSTNLMQDILRETEOFLNRLNTDTLA 111
 Db 69 KILGTGLVFPFACQVASLY-SFTLGLM-----PKGK-NQWEIFMEHVEEIIKQISTVARN 122
 QY 112 RVNAELEGLOANIREFNQOVNFNPTQNPVPLSIT-SSVNTMOQLFLNRLPQFRVQGYQ 170
 Db 123 KALTDKGLGDLALAYHDSLESWGVRNNTARSVVKSOYIALELMFVKQLPFAVSSEE 182
 QY 171 LLLLPLFAQAMHLSFIRDVVLNADEWIGISAATLRTYONVLYKNVTTESYNYCINTYOTA 230
 Db 183 VPLPIYAAQANLHLLLDASIFCKEGLWSSEISFTYNQVERAGYSCHCVKYSTG 242
 QY 231 FRGL-NTRLHML-----EFTYMLNVFEYVSWLSFKYQSLVSSGANL-----YASGSGP 282
 Db 243 LNNLRTNAESWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTQAQTRVYTDAGT 302
 QY 283 QQTQ-SFTSQDW-----PPL-----YSLFQVNSN-YVLNGFSG 313
 Db 303 VHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYNNMWGG 362
 QY 314 ARLTQTFNIGLPGTTTTTHALLAARVNYSGVSGDICAENQNFSCSTELPPLLPFV 373
 Db 363 HKL-EFTIGTGLNIST-----QGSNTSINPVTLPFT 394
 QY 374 RSWLDSGDRGGVNTV-----NQQ--TESFESTLGRGCAFTARGNSNFPD 419
 Db 395 SRDVYRTSLAGLNLFLTPQVNGVRVDFHVKFVTHPIAS-----DNFYYPG 441
 QY 420 YFIRNISGVPLVRNEDLRPLHYNEIRNIESPGTQGLRAYMVSVHNRKNLYA-VHE 478
 Db 442 Y-----AGITQLQDSENELPEATQGPYNEYSHRLSHG--LISASHVAKALYSWTHR 494
 QY 479 NGTMHLAPEDYTGFTISPIHATQV-----NNQTRTFISEKFG-NOGDSLRFPQSNTTA 531
 Db 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAARVGPFTGDIIL--RTWTGT 543
 QY 532 RYTLRGNG-----SYNLYRVSSLGNSITRTVINGRVYASNTVNTTNDGVNDNGARF 586
 Db 544 FGDIVRNIPFPAQRYRIRYASTDLOFTSINGKAINQGNFSATNR-----GED 596
 QY 597 LDINMGVNASDNTNVLVDINVT-----FNSGTQFELNMIMVPTNL 628
 Db 597 LDYKTRVGTFTFPFLDQVOSTFTIGAMNFSNGEVYIDRIEFVPEV 645

RESULT 10

C1BD_BACTZ
 ID_C1BD_BACTZ STANDARD; PRT; 1231 AA.
 AC Q9ZAZ5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidicidal crystal protein crylbd (insecticidal delta-endotoxin
 DE CrylB(d)) (crystalline entomocidal protoxin) (140 kDa crystal protein).
 GN CrylBD OR CrylBD OR CrylAI OR CrylE.
 OS Bacillus thuringiensis (subsp. wuhanensis).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=52024;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-525;
 RX MEDLINE=20153386; PubMed=10688690;
 RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
 RT "Cloning of two new cry genes from Bacillus thuringiensis subsp.
 RT wuhanensis strain";
 RL Curr. Microbiol. 40:227-232 (2000).
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLOUTELLA
 CC XYLOSTELLA.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
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 CC
 CC EMBL; U70726; AAD10292.1; -;
 DR HSP; P02965; ICIY.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR Pfam; PF00555; endotoxin; 1.
 DR Pfam; PF03944; endotoxin_C; 1.
 DR Pfam; PF03945; endotoxin_N; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 1231 AA; 139654 MW; 129A0371CDBBE52 CRC64;

Query Match 9.9%; Score 327.5; DB 1; Length 1231;
 Best Local Similarity 23.3%; Pred. No. 2.9e-14;
 Matches 155; Conservative 101; Mismatches 249; Indels 161; Gaps 29;
 QY 52 PIVGTSSFLKKGSLGKILSLGLIPSGSTNLMQDILRETEOFLNRLNTDTLA 111
 Db 73 PFAGLASFSFLVG-----ELW-----PSG-RDPWEIFLEHVEQLRQOUTENRN 118
 QY 112 RVNAELEGLOANIREFNQOVNFNPTQNPVPLSITSSVNTMOQL-FLNRLPQFRVQGYQ 170
 Db 119 TAIARLEGLGRGYSVQAQLETLWLDNRDARSIIILRYVVALELDTITAIPLFRINEE 178
 QY 171 LLLLPLFAQAMHLSFIRDVVLNADEWIGISAATLRTYONVLYKNVTTESYNYCINTYOTA 230
 Db 179 VPLLMVYAAQANLHLLLDASLFGSEWGNASDVNQYQEQYRYTEESYHNCVQWYNTG 238
 QY 231 FRGL-NTRLHML-----EFTYMLNVFEYVSWLSFKYQSLVSSGANL-----YASGSGP 282
 Db 239 LNNLRTNAESWVRYNQFRDMLVLDLVALFSPYDTRTYPTINTSAQLTREYTDPIGR 298
 QY 283 QQTQ-SFTSQDW-----PPL-----YSLFQVNSN-YVLNGFSG 313
 Db 299 TNAPSGFASTNWFNNNAPSFAIEAALFRPHLLDFPEQLTIYSSASRWSSTQHMNVWG 358
 QY 314 ARLTQTFNIGLPGTTTTTHALLAARVNYSGVSGDICAENQNFSCSTELPPLLPFV 373
 Db 359 HRL--NFRPIGGTLNTST-----QGLTNNTSINPVTLPFT 391
 QY 374 RSWLDSGDRGGVNTV-----NQQ--TESFESTLGRGCAFTARGNSNFPD 426
 Db 392 SRDVYRTSLAGLNLFLTPQVNGVRVDFHVKFVTHPIAS-----DNFYYPG 441
 QY 427 GYPLVVRNEDLRPLHYNEIRNIESPS-----GTFPG--LRAYMVS-VH-----467
 Db 442 GVGIQLFDSSETLPETTERPNYESYSHRLSHLIGLIGNTLRAPVYVSWTHRSADRTNTIG 501
 QY 468 -NRKNVIYVHE-----NGTMHLAPEDYTGFTISPIHATQVNNOTFTFISEKGNQDLSL 522
 Db 502 PNRITQIPAVKGRFLFNGSVI--SGFGTGGDVRNLRNNGNIGNQYI-----EV 550
 QY 523 RFEQSTNTARTYTLRGNSYNLYRVSSLGNSITRTV--NGRVYASNTVNTTNDGVND 581
 Db 551 PIQFTSTSTRYVR-----VRVASYTSELNVLNGLNSSIFTWTLPATAASLDNLQS 601
 QY 582 NGARFLDIN-----MGNVVA-----SDNTNVLVD-----INVTNSGTQFEL-----MNI 621
 Db 602 GDFGYVEINNAFTSATCNIVGARNFSAEVIIDREFIPVTATFAEYDLERAQAVNA 661
 QY 622 MFVPTN 627



Db 662 LFTSTN 667

RESULT 11

ID	CLID_BACTU	STANDARD	PRT	719 AA.
AC	Q9XDL1			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pesticidal crystal protein cryII(d) (Insecticidal delta-endotoxin			
DE	CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).			
GN	CryII(d) OR CRYII(D) OR NCRVYV.			
OS	Bacillus thuringiensis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
NCBI	TaxID=1428;			
[1]	_TaxID=1428;			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=BR30;			
RC	MEDLINE=20374042; PubMed=10919402;			
RX	Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;			
RT	"Cloning of a new Bacillus thuringiensis cryII-type crystal protein			
RT	gene.";			
RL	Curr. Microbiol. 41:65-69(2000).			
CC	-!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT			
CC	EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE. ACTIVE ON PLUTELLA			
CC	XYLOSTELLA AND ON BOMBYX MORI.			
CC	-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING			
CC	SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART			
CC	OF THE SPORE COAT.			
CC	-!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE			
CC	N-TERMINUS.			
CC	-!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; AF047579; RAD44366.1; -.			
DR	HSSP; P02965; 1CIY.			
DR	InterPro; IPR001178; Endotoxin.			
DR	InterPro; IPR005638; endotoxin_C.			
DR	InterPro; IPR005639; endotoxin_N.			
DR	Pfam; PF00555; endotoxin_1.			
DR	Pfam; PF03944; endotoxin_C; 1.			
DR	Pfam; PF03945; endotoxin_N; 1.			
KW	Toxin; Sporulation.			
SEQUENCE	719 AA; 81403 MW; F335F5689D3B0C45 CRC64;			
Query Match	9.8%; Score 325; DB 1; Length 719;			
Best Local Similarity	22.5%; Pred. No. 2e-14;			
Matches	145; Conservative 101; Mismatches 255; Indels 144; Gaps 27;			
QY	52 PIVGTVSSFLKKVGSGLGKRLSELWGLIFPFGSGTNLMQDILRETFQFLNRLNTDTLA 111			
DB	77 PFAQGVAS-----LYSFILGLW----PKGKSQ-WEIFMHEVELINQKISTYARN 122			
QY	112 RYNAELGLEQANIREFNQVDNFL-NPTQNPVPLSITSSVNTMOOLFNLRLPQRFVQYQ 170			
DB	123 KALADLKLGLDGLAVYHSHLESLENIENRNRVRSVVRKQYIALELMFVQKLPSPFVSGEE 182			
QY	171 LLLPLFQAAMNHLSPTRDVLVNADEWIGISAATRLQNYLQNYLTYEYSNYCINTYQTA 230			
DB	183 VPLLPIYAQAANLHLLLRDASIFCKEGLSESEISTFYNRQSSQTOEYSDCYSEWNTG 242			
QY	231 ---FRGLN----TRHDMLEPRTYFNFLVFEVSVLSLFFKYSQSLIVSSGANL-----YASG 279			
DB	243 LNLRLGTTNAESWVRYN---QFRDRLTMLDLVALFPSSYDTRMYPPIPTSAQLTREVYTD 299			

280 SGP-QOOTSFTSQDW-----PFL-----YSLFQVNSN-YVLNG 311

300 IGVVHPNASFASTTWYNNNAPSFTIEAAVVRNPHLLOFLEQVTIYSLSRWSNTQYNNM 359

311 FSGARLTQTFPNIGLPGTITTHALLAARVNVSGVSGDIGAENVQNFSCSTFLPPLLT 370

360 WGHKL--BFTTIGGLTNT-----QGSTNTSINPVL 391

371 PFVRSLDGSGRGGVNTVT-----NMQ--TESPESTLGLRCGAFTARGNSNY 416

392 PTFSDRVRTESLAGLNFLQPVNGVRVDFHMKFVTHPIAS-----DNFY 438

417 FPDYFIRNISGVPVLRNEDLRRPLHYNEIRNISPSGTPGGLRAYVMVSHNRKNIYA- 475

439 YPGY-----AGIGTQLODSENELPPTTGPQNYESYSHRLSHIG--LISASHVKALVYSW 491

476 VHENGTMHLPEDYTGFTISPIHATQV-----NNQTRTFISEKFGNGQSLRPEQSNT 529

492 THRSA-----DRTN-TINSDSITQIPLVKAFNLPDSGASVVRGPGTGGDI-LQRTNT 541

530 TARYTLRNGN-----SYNLVLRVSSLSNSTIRVTINGRVYTASNVTNTTNDGVNDNGA 584

542 GTFGDIRVNNPPFAQRRLRIRYASTTNLEFHTSINGKAINQGNFSATMR-GEEDLYK 600

585 RFLDINMGVNASDNTNVPDLINV-TFNSGTQFELMNMFPVPTNL 628

601 ARTVGTTPPSFSAQSTFTTIGAWNFSGLNEVVIDRIEFVPEV 645

RESULT 12

ID	CLIB_BACTE	STANDARD	PRT	719 AA.
AC	Q45709;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pesticidal crystal protein cryIb (Insecticidal delta-endotoxin			
DE	CryI(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).		</	

Db 359 RFPVSSNF-MDYVSGHTLRSSLYNDSAVQEDSYGLITTTTRATINPGVDGNNRIESTAVDF 417
Qy 353 -----AVFNQFSCSTFLPPLLTPFVRSWLDGSD---RGGVNTV---TNMQTESFESTLG 402
Db 418 RSALIGIYGVN-----RASFPVGGFLFNGTTSPANGGCRDLYTNDLPDEST-- 465
Qy 403 LRCAFTARGNSYFPDY-----FIRNIGVPLV---RNEDLRRLPHYNEIRNIESPS 453
Db 466 ---GSSTHRLSHVTFQFNQAGSIANAGSVPTVYVWTRDVLNNTITPNRITQLP--- 519
Qy 454 GTPGGLRAYMVSVHNRKNNIYAVHENGTMTHLAPEDVTGFTTISPIHATQVNNQTRFISE 513
Db 520 -----LVKA-----SAPVSGITVLKGP-----GFT----- 539
Qy 514 KFGNQDLSRFEQSNITARYTLRGNGS-----YNLYRVSLSGNSITRVIN-----GRV 564
Db 540 ---GGGILARTTNGTGF---TLRVTVNSPLTQQYRLAVRFPASTGNSFIRVLRGGVSGDV 593
Qy 565 YTASNVN-----TTT-----NDGVNDNGARFLD--- 588
Db 594 RLGSMTNRGOELTVESFTREFTTGPFPNPFPTTQAEILLTVNAEGVSTGGEYIDRIE 653
Qy 589 ---INMGVNVASD-----NTNVPLDINVT 609
Db 654 IVPVNPAREAEEDLEAAKKAVASLFTTRDGLQNVNT 690

RESULT 14
C7AB_BACUA STANDARD; PRT; 1138 AA.
AC Q45707;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIaB (Insecticidal delta-endotoxin
DE CryIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN CRY7AB OR CRYVIIA(B).
OS Bacillus thuringiensis (subsp. dakota).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132268;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD511;
RT "Coleopteran-active Bacillus thuringiensis isolates and genes encoding
RT coleopteran-active toxins";
RL Patent number US5286486, 15-FEB-1994.
CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC
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CC
CC EMBL; U04367; AAA21120.1; -;
CC HSPSP; P07130; 1DLC.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC Pfam; PF00555; endotoxin; 1.
CC Pfam; PF03944; endotoxin_C; 1.
CC Pfam; PF03945; endotoxin_N; 1.

KW Toxin; Sporulation.
SQ SEQUENCE 1138 AA; 129778 MW; 01DF7072C074CE88 CRC64;
Query Match 9.2%; Score 306; DB 1; Length 1138;
Best Local Similarity 20.0%; Pred. No. 7.3e-13;
Matches 135; Conservative 109; Mismatches 222; Indels 208; Gaps 25;
Qy 52 PIVGTSSVFLKKVGLIKRILSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTLA 111
Db 76 PGASPTITNFKL-----ITGLLWPH-NKNINWDEFTEVETLIEQIEQVARN 121
Qy 112 RVNAELEGLOANRENNQVDNPLNQVPLS-ITSSVNTMQQLFLNLPQFRVQYQ 170
Db 122 KALAELEGGLNLTIIYQALDELWLNPPDPATITRVIRDLRDLALFESYMPFRVAGYE 181
Qy 171 LILPLPFAQANMHLNFIRVDVNLNADWEGISAATLRTQYKLYKNTYTESNYCINTYQTA 230
Db 182 IPLLTVYAQAANLHALLADSDLYDGKGFQNNIENYNRQKHISEYNSHCVKYNNG 241
Qy 231 FRGLNRLHDM- ---EFRTYMLNVEFYVSIWLSFKYQSLVSSGANLYVSGSGPQQTQ 286
Db 242 LSRLLNGSTVEQWYNFRFRREMILMVLDIAAVFPYD-----ET----- 278
Qy 287 SFTSQDWPELYSLFQVNSYVNLNGFSGARLTQTQTFNIGGLPGTTTHALLAARVNYSGV 346
Db 279 ---PRYSM-----ET-----STQLTREVVYTDPISL- -I 303
Qy 347 SSGDIGAVFNQFSCSTFLPPLLTPFVRSWLD----- 378
Db 304 SNPDIGPFSQMENTA-----FRTPLVDYLDLYIYTSKYKAFSHEIQDPLFYWCVKV 358
Qy 379 --SGSDRGVNTVNMQTESFESTLG-LRCGAFARTAGNSNYFPDYFIRNIGSVPLVVRNE 435
Db 359 SPKKSQSNLYT-----TGIYKTSVGISSGAYSPRGNDIY-----RTLAPSVVV- 404
Qy 436 DLRRPLHYNEIRNIESPS-GTPGGLRAYMVSVHNRKNNIY-----AVHE 478
Db 405 -----YPTQNYGVEQVEFYGVKG-----HVHGRDNKYDLYDSIDQLPPDGEPHE 452
Qy 479 -----NGTMHILAPEDVTGFTTISPIHATQVNNQTRTPISEKFGNQDLSRFEQSNNTA 531
Db 453 KYTHRLCHATAISKSTPDYDNATI-PFSW-----THRSAYEYNIYRNPKIKKIPAVK 504
Qy 532 RYTL-----RG-NG-----NSYNLYLRVSSLSGHNSTIR 557
Db 505 MYKLDDLSTVVKVPGFTGGDLVKRSGNGYIGDIKATVNSPLSKYRVRVRYATSVSGLFN 564
Qy 558 VTINGRVYASNVNTT---TNNDGVNDNGARFLDINNMGVNVASDNTVPLDINVT-FNSGT 614
Db 565 VFINDSIALQKNFQSTVETIGEGKDLTYGSGFYIYSTTTIQFPNHPKTLHLNHLNNS 624
Qy 615 QFELMNMIFVPTNL 628
Db 625 PFYVDSIEFIPVDV 638

RESULT 15
C1BE_BACTU STANDARD; PRT; 1227 AA.
ID -C1BE_BACTU
AC O85805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIb (Insecticidal delta-endotoxin
DE CryIb(e)) (Crystalline entomocidal protoxin) (139 kDa crystal protein).
GN CRY1BE OR CRYIB(E) OR 158C2B.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-18872 / PS158C2;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 16:14:45 ; Search time 21 Seconds
(without alignments)
2894.219 Million cell updates/sec

Title: US-10-040-906A-2

Perfect score: 3314

Sequence: 1 MNNVLNNGRTTICDAYNVVA.....CTQFELNIMVFNLPPIY 632

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3048.5	92.0	633	2 C32053	parasporal crystal
2	3010.5	90.8	633	2 D32053	parasporal crystal
3	2545	76.8	622	2 S17402	parasporal crystal
4	336.5	10.2	643	2 A43647	parasporal crystal
5	327.5	9.9	719	2 I39815	insecticidal prote
6	324.5	9.8	719	2 S25383	parasporal crystal
7	324.5	9.8	719	2 I39814	insecticidal prote
8	310.5	9.4	719	2 I40590	cryv465 protein -
9	307	9.3	1157	1 S49247	parasporal crystal
10	294.5	8.9	1176	2 A48970	parasporal crystal
11	282.5	8.5	1176	2 J70241	parasporal crystal
12	280.5	8.5	934	2 A42798	parasporal crystal
13	277.5	8.4	380	2 B42459	hypothetical prote
14	277	8.4	1181	2 A41052	parasporal crystal
15	276.5	8.3	1176	2 J32219	parasporal crystal
16	275.5	8.3	1228	2 S00873	parasporal crystal
17	273	8.2	1176	2 A26513	parasporal crystal
18	271.5	8.2	1176	2 A26217	parasporal crystal
19	271.5	8.2	1176	2 S02125	parasporal crystal
20	269	8.1	1155	2 S02134	parasporal crystal
21	268	8.1	1155	2 J00002	parasporal crystal
22	268	8.1	1156	2 A29125	parasporal crystal
23	267.5	8.1	1178	1 UBSXHX	parasporal crystal
24	267	8.1	1155	2 I39838	parasporal crystal
25	265	8.0	1174	2 A42459	parasporal crystal
26	264.5	8.0	1160	2 I40589	parasporal crystal
27	264	8.0	1174	2 S32649	parasporal crystal
28	262.5	7.9	1156	2 A29838	parasporal crystal
29	261.5	7.9	1172	2 S32689	parasporal crystal

30 259 7.8 1165 2 S11446 parasporal crystal
31 259 7.8 1177 2 A49785 parasporal crystal
32 255.5 7.7 649 1 JH0261 parasporal crystal
33 253 7.6 618 2 S11445 parasporal crystal
34 253 7.6 1138 2 A48944 parasporal crystal
35 250 7.5 652 2 A27323 parasporal crystal
36 249.5 7.5 652 2 I39811 parasporal crystal
37 247.5 7.5 659 2 S10228 parasporal crystal
38 244 7.4 1160 2 S32647 parasporal crystal
39 237 7.2 613 2 JC6033 mosquitocidal prot
40 230.5 7.0 655 2 JC7140 protoxin - Bacillu
41 229.5 6.9 1189 2 S00944 parasporal crystal
42 225 6.8 823 2 S04181 parasporal crystal
43 218.5 6.6 1171 2 A37829 parasporal crystal
44 218.5 6.6 1171 2 I40572 parasporal crystal
45 216 6.5 1154 2 S39536 parasporal crystal

ALIGNMENTS

RESULT 1
C32053
parasporal crystal protein B1 - Bacillus thuringiensis subsp. kurstaki
N:Alternate names: parasporal crystal protein P2
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 15-Oct-1999
C:Accession: C32053; A29913
R:Widner, W.R.; Whiteley, H.R.
J. Bacteriol. 171, 985-974, 1989
A:Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis sub
A:Reference number: A32053; MUID:89123178; PMID:2914879
A:Accession: C32053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-633 <WID>
R:Dolan, W.P.; Dankocsk, C.C.; Gilbert, M.P.; Gawron-Burke, M.C.; Groat, R.G.; Carlo
J. Biol. Chem. 263, 561-567, 1988
A:Title: Amino acid sequence and entomocidal activity of the P2 crystal protein. An inse
A:Reference number: A29913; MUID:88087146; PMID:3121615
A:Accession: A29913
A:Molecule type: DNA
A:Residues: 1-587, 'FRY' <DON>
C:Genetics:
A:Gene: cryBI

Query Match 92.0%; Score 3048.5; DB 2; Length 633;
Best Local Similarity 90.7%; Pred. No. 6.7e-200;
Matches 574; Conservative 34; Mismatches 24; Indels 1; Gaps 1;

Qy 1 MNNVLNNGRTTICDAYNVVAHDPSPFHKSLDTIRKEMWKRTHDLSLYVAPIVGTVSSP 60
Db 1 MNNVLNNGRTTICDAYNVVAHDPSPFHKSLDTIRKEMWKRTHDLSLYVAPIVGTVSSP 60
Qy 61 LLKKVGSLLIGKRLSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTTLARVNAEGL 120
Db 61 LLKKVGSLLIGKRLSELWGLIFPSSGNTLMQDILRETEQFLNQLRNTDTTLARVNAEGL 120
Qy 121 QANIRENQVDNPLNPTQNPVPLSITSSVNTMOQLNRLPQFRVQYQLLLPLFAQA 180
Db 121 QANIRENQVDNPLNPTQNPVPLSITSSVNTMOQLNRLPQFRVQYQLLLPLFAQA 180
Qy 181 ANMHLSTIRVDVLNADBWGISAATLRYQYLNKNTTYSNYCINTYTQAFGLNTRLHD 240
Db 181 ANMHLSTIRVDVLNADBWGISAATLRYQYLNKNTTYSNYCINTYTQAFGLNTRLHD 240
Qy 241 MLEFRTYMLNVPFYVSIWSLFKYQSLVSSGANLYASGGSPQQTQSTQDWPFLYSLF 300
Db 241 MLEFRTYMLNVPFYVSIWSLFKYQSLVSSGANLYASGGSPQQTQSTQDWPFLYSLF 300
Qy 301 QVNSNYLVNFGSGARLTQTFPNIGGLGCTTTTHALLAARVNYSGVSSGDIGAV-FNQNF 359
Db 301 QVNSNYLVNFGSGARLTQTFPNIGGLGCTTTTHALLAARVNYSGVSSGDIGAV-FNQNF 359

QY 283 QQTQ-SQTSQDM-----PFL-----YSLFQVNSN-YVLNGFSG 313
Db VHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMGG 362
QY 314 ARLTQTFNPNGGLPGTTHALLAARVNYSGVSSGDIQAVFNQFSCSTPLPPLTPFV 373
Db 363 HKL--EFTIGTGLNIST-----QGSTNTSINPVTLPFT 394
QY 374 RSWLDSGDRGGVNTV-----NQW--TESFESTLGLRCGAGTARGNSNYPDP 419
Db 395 SRDYRTESLAGNLFLTPQVNGVPRVDFHWKFVTHPIAS-----DNFYYPG 441
QY 420 YFIRNIGSVPLVRNEDLRPLHYNEIRNIESPSTGGLRAYMVSVHNRKNYIA-VHE 478
Db 442 Y-----AGIGTQLODSENELPEATGQPNYESYSHRLSHIG--LISASHVKAIVYSWTHR 494
QY 479 NGTMHLAPEDYGTFTSPIHATQV-----NNQTRTFISEKFG-NOQDSLRFEOSNTTA 531
Db 495 SA-----DRTN-TIEPNSITQPLVKAFLNLSGAAVVRGPGFTGGDILR--RTWTGT 543
QY 532 RYTLRGNGN-----SYNLYLRVSSLGNSITRVINGRVYTASNVTNTTNDGVNDNGARF 586
Db 544 FGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596
QY 587 LDINMGNVASDNTNVPLDINVT-----FNSGTQFELMNMIFVPTNL 628
Db 597 LDYKTRTVGTTPPFLDVQSTFTIGAMFNSSGNEVYIDRIEFPVFEV 645

RESULT 6

I39814
parasporal crystal protein cryIIa1 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV
C:Species: Bacillus thuringiensis
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 01-Dec-2000
C:Accession: S25383
R:Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin
A:Reference number: S25383; MUID:92269582; PMID:1588820
A:Accession: S25383
A:Molecule type: DNA
A:Residues: 1-719 <TAI>
A:Cross-references: EMBL:X62821; NID:g40289; PIDN:CAA44633.1; PID:g40290
C:Genetics:
A:Gene: cryV
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 9.8%; Score 324.5; DB 2; Length 719;
Best Local Similarity 22.8%; Pred. No. 3.5e-14;
Matches 162; Conservative 102; Mismatches 272; Indels 173; Gaps 32;
QY 21 HDPSFEHK-----SLDTIRKEM-MEWKRTDH-----SLY--VAP----- 52
Db 9 HQSFSSNAKVDKISTDSKNETDIELQNIHEDCLKMSEYENVEFPVASTIQTGIGIAG 68
QY 53 -IVGTVSSFLKKVGLSKRILSELWGLIFPPSGSTNLMQDILRETEQFLNQLRLTDTLA 111
Db 69 KILGTGVPPAGQVASYL-SFILGELW---PKGK-NQWEIFMEHVEEIIINQISTVARN 122
QY 112 RVNALEGLQANIREFNQVDNFINPTONPVLPSIT--SSVNTMQOLFNLRLPQFRVQGYQ 170
Db 123 KALTDKLGGLDALAVYHDSLSGVNRRNTRARSVVKVSYQIALELMFVKQLPSFAVSGEE 182
QY 171 LLLPLPFAQAANMHLSPFRDVLNADWEGISAATLRTYONLKNYTTYSNYCINTYOTA 230
Db 183 VPLPIYQAANLHLLLRDASIFCKEWGLSSSEISTFYNRQVERAGDYSHCVKWTGT 242
QY 231 FRGL-NTRLHDML---EFTYTMFLNVFVYIWSLFKYQSLVSSGANL-----YASGSGP 282
Db 243 LNNLRGTNAESWRYNQFRDWTLMVLVALFPSYDTQMPYIKTKAQLTREVYTDAGT 302

QY 283 QQTQ-SQTSQDM-----PFL-----YSLFQVNSN-YVLNGFSG 313
Db VHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMGG 362
QY 314 ARLTQTFNPNGGLPGTTHALLAARVNYSGVSSGDIQAVFNQFSCSTPLPPLTPFV 373
Db 363 HKL--EFTIGTGLNIST-----QGSTNTSINPVTLPFT 394
QY 374 RSWLDSGDRGGVNTV-----NQW--TESFESTLGLRCGAGTARGNSNYPDP 419
Db 395 SRDYRTESLAGNLFLTPQVNGVPRVDFHWKFVTHPIAS-----DNFYYPG 441
QY 420 YFIRNIGSVPLVRNEDLRPLHYNEIRNIESPSTGGLRAYMVSVHNRKNYIA-VHE 478
Db 442 Y-----AGIGTQLODSENELPEATGQPNYESYSHRLSHIG--LISASHVKAIVYSWTHR 494
QY 479 NGTMHLAPEDYGTFTSPIHATQV-----NNQTRTFISEKFG-NOQDSLRFEOSNTTA 531
Db 495 SA-----DRTN-TIEPNSITQPLVKAFLNLSGAAVVRGPGFTGGDILR--RTWTGT 543
QY 532 RYTLRGNGN-----SYNLYLRVSSLGNSITRVINGRVYTASNVTNTTNDGVNDNGARF 586
Db 544 FGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596
QY 587 LDINMGNVASDNTNVPLDINVT-----FNSGTQFELMNMIFVPTNL 628
Db 597 LDYKTRTVGTTPPFLDVQSTFTIGAMFNSSGNEVYIDRIEFPVFEV 645

RESULT 7

I39814
insecticidal protein cryVI - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C:Accession: I39814
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I39814
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: GB:L36338; NID:g540281; PIDN:AAC36999.1; PID:g540282
C:Genetics:
A:Gene: cryVI
C:Superfamily: parasporal crystal protein

Query Match 9.8%; Score 324.5; DB 2; Length 719;
Best Local Similarity 22.8%; Pred. No. 3.5e-14;
Matches 162; Conservative 102; Mismatches 272; Indels 173; Gaps 32;
QY 21 HDPSFEHK-----SLDTIRKEM-MEWKRTDH-----SLY--VAP----- 52
Db 9 HQSFSSNAKVDKISTDSKNETDIELQNIHEDCLKMSEYENVEFPVASTIQTGIGIAG 68
QY 53 -IVGTVSSFLKKVGLSKRILSELWGLIFPPSGSTNLMQDILRETEQFLNQLRLTDTLA 111
Db 69 KILGTGVPPAGQVASYL-SFILGELW---PKGK-NQWEIFMEHVEEIIINQISTVARN 122
QY 112 RVNALEGLQANIREFNQVDNFINPTONPVLPSIT--SSVNTMQOLFNLRLPQFRVQGYQ 170
Db 123 KALTDKLGGLDALAVYHDSLSGVNRRNTRARSVVKVSYQIALELMFVKQLPSFAVSGEE 182
QY 171 LLLPLPFAQAANMHLSPFRDVLNADWEGISAATLRTYONLKNYTTYSNYCINTYOTA 230
Db 183 VPLPIYQAANLHLLLRDASIFCKEWGLSSSEISTFYNRQVERAGDYSHCVKWTGT 242
QY 231 FRGL-NTRLHDML---EFTYTMFLNVFVYIWSLFKYQSLVSSGANL-----YASGSGP 282
Db 243 LNNLRGTNAESWRYNQFRDWTLMVLVALFPSYDTQMPYIKTKAQLTREVYTDAGT 302

QY 283 QQTQ-SFTSQDW-----PFL-----YSLFQVNSN-YVLNGFSQ 313
DB 303 VHPSPSTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMGG 362
QY 314 ARLTQTFNIGLPGTTHALLAARVNYSGVSSGDIGAVNQFNQFSGTFLPPLTPPV 373
DB 363 HKL--EFTIGTLMIST-----QGSNTSINPVTLPFT 394
QY 374 RSLWDSGDRGQVNTV-----NWO--TESPESTLGLRCGAFARGNSNYPPD 419
DB 395 SRDVYRTESLAGNLFLTPQVNGVPRVDFHMKFVTHPIAS-----DNFYVPG 441
QY 420 YFIRNISGVPLVRNEDLRPLHYNEIRNIESPSTGGLRAYMVSVNRKNIIYA-VHE 478
DB 442 Y-----AGTGLQDSENELPEATGQPNYESYSHRLSHIG--LISASHVKALVYSWTHR 494
QY 479 NGTMIHLAPEDYGTIPPIHATQV-----NNQRTFISEKFG-NOGDSLRFEOSNTTA 531
DB 495 SA-----DRTN-TIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILR--RTNTGT 543
QY 532 RYTLRGNG-----SYNLYRVSSLSGNSIRTVINGRVYTSNVTNTNNDGVNDNGARF 586
DB 544 FGDIRVNINPPAQRVYRIRVASTTDLQFHTSINGKAINQGNFSATMNR-----GED 596
QY 587 LDINMGNVASNTNVPDLNVT-----FNSGTQFELMNMFPVTNL 628
DB 597 LDYKTRTVGFTTPPSFLDVQSTFTIGAWNFSSGNEVYDRIEFVPEV 645

RESULT 8

I40590
Cryv465 protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-Aug-1999
C:Accession: I40590
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A:Title: Distribution of cry-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I40590
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g467235
C:Genetics:
A:Gene: cryV465
C:Superfamily: parasporal crystal protein

Query Match 9.4%; Score 310.5; DB 2; Length 719;
Best Local Similarity 22.7%; Pred. No. 3.1e-13;
Matches 153; Conservative 116; Mismatches 259; Indels 145; Gaps 34;
QY 27 EHKSLDTRKEWMEKRDHSLIYA-PIVGTVSSFLKKVGLIKRILSELWGLIFPSG 85
DB 47 EHESID-----PVSASTITQGTGIGAKILGLTGVFPAGQIASLY-SFILGELW-----PKG 97
QY 86 STNLMQDILRETEQFLNRLNTDTLARNVAELEGQANIREFNQVDNPLNTPQNPVLS 145
DB 98 KSO-WEIPEWHEVEEINIKILTYARNKALSDURLGLDALAVHESLESWEVNRNTRRS 156
QY 146 IT-SSVNTMQQLFLNRLPQFVQYQLLLPLFAQAANMHLISFIRDVVLNADWEGISAAT 204
DB 157 VVKNQYIALELMFVKLPSPFAVSGEVPPLPIYAQAANLHLLLRDASIFGKEMGLSASE 216
QY 205 LRTYQNYLKNYTTESVNCINTYQTA---FRLNTRLHML-EFTYMFNLFVFEVSIWS 260
DB 217 ISTFNQVRETRDYSCHIKWYNTGLNNLRGTNAKSWVRNQFRKDMTLMVLDIVLALFP 276
QY 261 LFKYQSLK--VSSGANL---YASGGP-QQTQSTSDWPPLYSLFQVNSVYVNGFSQ 313
DB 277 --SYDTLPIKTSQLTREVYTDAGTVHPNQAFSTTW-----YNNNAPSFAIE 326

QY 314 ARLTQTFNIGLPGTTHALLA-----ARVNYSGG--VSSGDIGAVNQFNQFSGTFLP 366
DB 327 AAVIRS-PHLDFLEKVTIYSLLSRWSNTQYNNMGGHRLSRPTGGALNT----- 376
QY 367 PLLFPFVRSWLDSDSGDGGVNTVNWOTESP-----ESTLGLRCGAFARGNSNYPP 418
DB 377 -----STQGSNTSINPVTLPQTSRDVYRTESLAGNL----- 409
QY 419 DYFIRNISGV-----LVVRNEDLRPLHY-----NEIRNIES--PSGTPG-- 457
DB 410 -FLTPQVNGVPRVDFHMKFPLPIASDN----FYLVGAGVGTQLQDSENELPETTQOP 464
QY 458 GLRAY-----MVSVNRKNIIYA-VHENGTHIHLAPEDYGTFTTPIHATQV----- 503
DB 465 NYESYSHRLSHIGLISASHVKALVYSWTHRSA-----DRTN-TIEPNSITQIPLVKA 515
QY 504 -NNQRTFISEKFG-NOGDSLRFEOSNTTARYTLRGNG-----SYNLYRVSSLSGNSNTI 556
DB 516 FNLSSGAAVVRGPGTGGDILR--RTNTGTGDIRVNINPPAQRVYRIRVYASTTDLQF 573
QY 557 RVTINGRVYTSNVTNTNNDGVNDNGARFLDINMGNVASNTNVPDLNVTN-TFNSGTQ 615
DB 574 HTSINGKAINQGNFSATMNR-GEGLDYKTRFTIGTTPPSFSDVQSTFTIGAWNFSSGNE 632
QY 616 FELNMIMPVTNL 628
DB 633 VYIDRIEFVPEV 645

RESULT 9

S49247
parasporal crystal protein cry9Ca1 [validated] - Bacillus thuringiensis
N:Alternate names: parasporal crystal protein cryIH
C:Species: Bacillus thuringiensis
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: A59350; S49247
R:Lambert, B.; Buysse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.;
Appl. Environ. Microbiol. 62, 80-86, 1996
A:Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity against
A:Reference number: A59350; MUID:96141404; PMID:8572715
A:Accession: A59350
A:Molecule type: DNA
A:Residues: 1-1157 <LAM>
A:Cross-references: EMBL:Z37527; NID:g547554; PIDN:CAA85764.1; PID:g547556
A:Experimental source: serovar tolworthi
C:Comment: This parasporal crystal protein, active against corn borer and other insects,
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 9.3%; Score 307; DB 1; Length 1157;
Best Local Similarity 23.4%; Pred. No. 1.1e-12;
Matches 163; Conservative 87; Mismatches 215; Indels 232; Gaps 34;
QY 52 PIVGTVSSFLKKVGLIKRILSELWGLIPPSGSTNLMQDILRETEQFLNRLNTDTLA 111
DB 87 PFSGQIVSFY-----QFLNTLW----PVNDTAIWEAFMRQVBEELVNOQITFARN 133
QY 112 RVNAELEGQANIREFNQVDNPL--NPTQNPVPLSITSSVNTMQQL-FLNRLPQPRVQ 167
DB 134 QALARLQGLGDSFNVYORSQNLWLDNRDTRN---LSVVRQAFTALDLPFVNAIPLFAVN 190
QY 168 GYQLLLPLFAQAANMHLISFIRDVVLNADWEGISAATLRTYQNYLKNYTTESVNCINTY 227
DB 191 GOQVPLLSVVAQAVNLHLLKQASLFGEGWGTQGEISITVYDRQLBELTAKYTYNCETWY 250
QY 228 QTA---PRGLNT-----RLHDMLEPRTYMFNLFVFEVSIWSLFKYQSLVSSGANLYASGS 280
DB 251 NTGLDRLRGNTESWLRYH---QPRENTLVLDVW---ALFPYYDV-----RLYPTGS 298
QY 281 GPQQTQS-FTS-----QDW-----PFLY-----S 298
DB 299 NPQLTREYVTDPIVFNPPANVGLCRRWGTNPYNTFSBLENAFTRPPLHLPRLNLSLTGSN 358


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Db 261 SOLTR-----EITNPVLENFDGFRGMAQRIEQINQPHMLDILNITITVDVHR 311
Qy 339 RVNYSGG--VSSGDIGAVNQFSCSTF-----LPPLLT----- 371
Db 312 GFNYWSGHQITASPVG-----FSGPEFAPFLFGNAGNAAPPVLVSLTGLGIFRTLSPL 365
Qy 372 FVRSWLDGSDRGVNTVNNQTESFESTLGRCAFTARGNSYFDPYFRINISGVPLV 431
Db 366 YRRILGSGPNNQELFVLDGTEFASLTNLPSTIYRQGT-----VDSLVDVIPPQ 417
Qy 432 VRNEDLARPLHY--NEIRNIESPSGTPGGLRAYVMVSVHNRK--NNIYAVHE----- 478
Db 418 DNSVPPRAGFHRLSHVMTLSQAAGAVYTLRAPTFHQHRSABFNIIIPSSQITQIPLTK 477
Qy 479 -----NGTMHLAPEDYGTFTISPIHATQVNNQTRTFISEKFGQDGLRFEQSNITARY 533
Db 478 STNLGSGTSVVKGP-----GFT-----GGDILR--RTSPQGIS 508
Qy 534 TLRGN-----GNSNLYLRVSSLSGNSTIRVTINGRVYVYASNVNTTNDGNDVNGARPLD 588
Db 509 TLRNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSAITMSS--GSNLSQSGFRT 567
Qy 589 INMGNVVASDNTNVPLDINV--TENSQTQFELMNMVEPTNL 628
Db 568 VGFTTPNFSGSVFTLSAHVFNSGNEVYDRIEFVPAEV 608
```

RESULT 12

A22798
parasporal crystal protein - *Bacillus thuringiensis*
C:Species: *Bacillus thuringiensis*
C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 01-Dec-2000
C:Accession: A22798
R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.
Gene 34, 243-251, 1985
A:Title: Nucleotide sequence coding for the insecticidal fragment of the *Bacillus thuringiensis* parasporal crystal protein
A:Reference number: A22798; MUID:85232070; PMID:2989108
A:Accession: A22798
A:Molecule type: DNA
A:Residues: 1-934 <SHI>
A:Cross-references: GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713
C:Comment: The authors translated the codon ACA for residue 264 as Ser.
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

```
Query Match 8.5%; Score 280.5; DB 2; Length 934;
Best Local Similarity 21.7%; Pred. No. 5.1e-11;
Matches 152; Conservative 104; Mismatches 272; Indels 173; Gaps 29;

Qy 6 NNGRTTICDAYNVVAHDPFSEKSLDTIRKEMMEKRT--DHSLYVAPIVGTVSSFLK 63
Db 3 NNPINECIPNCLSL-----NPEVVLGGERIETGYTPIDISL-----SLTQFLLS 48
Qy 64 K-----VCSLIGKRLSELGLIFPSGNTLMQDILRETEQPLNORLNTDTLARVNALEG 119
Db 49 EFVPGAGFVLG--LVDIWIGFGRS---QWDAFLVQTEQLINQRIEFARNAQISLEG 102
Qy 120 LQ-----ANIREFNQVDNLTQNPVLSITSSVNTMQQLFLNRLPQFRVQYQLL 172
Db 103 LSNLYQIYASFRWE-----ADTPALREEMRIQFNNDNSALTAPLFAVQNTQVP 156
Qy 173 LPLFAQAANHLFSIRDVLNADWGISATLRTYQNLKNTYTESNYCINTYQTAFR 232
Db 157 LLSVYVQAANHLVLSDVSVFGQWGFDAATINSRYNDLTRLIGNYTDVAVRWYNTGLE 216
Qy 233 ---GLNTRLHML---BFTYMFNLVFEYVSIWLFKYQSLVSSGANLYASGGPQQTQ 286
Db 217 RVWGPDSR--DWRYNQFRRELTTLVDLVALFS-----NYDSRRYPIRTV 260
Qy 287 SFTSQDWPFLYSLFQVNSNYLVNGFSGA-----RLTQTP--PNIGLPGTTTHALLAA 338
Db 261 SOLTR-----EITNPVLENFDGFRGMAQRIEQINQPHMLDILNITITVDVHR 311
```

RESULT 13

B42459
hypothetical protein 2 (cryIF 3' region) - *Bacillus thuringiensis* (strain aizawai) (frag
C:Species: *Bacillus thuringiensis*
C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 30-Sep-1993
C:Accession: B42459
R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-3976, 1991
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene from
A:Reference number: A42459; MUID:91286178; PMID:2061280
A:Accession: B42459
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <CHA>
A:Cross-references: GB:M63897
C:Superfamily: parasporal crystal protein

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Query Match 8.4%; Score 277.5; DB 2; Length 380;
Best Local Similarity 26.3%; Pred. No. 2.1e-11;
Matches 100; Conservative 66; Mismatches 135; Indels 79; Gaps 19;

Qy 21 HDPSFEHK-----SLDTIRKEM-MEWKRTDH-----SLY--VAP----- 52
Db 9 HQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKISEVENPEPVFASTIQTGISAG 68
Qy 53 -IVGTVSSFLKVKVSLIGKRIILSELWGLIFPSGNTLMQDILRETEQPLNORLNTDTLA 111
Db 69 KILGTILVPPAGVVASLY--SFILGELW----PKGK-NQWEIFMEHVEEIIKQISTYARN 122
Qy 112 RVNAELGQANIREFNQVDNLTQNPVLSIT--SSVNTMQQLFLNRLPQFRVQYQ 170
Db 123 KALTDLKGLDALAVYHSESLESVMGNKNTARSVVKSQVIALELMFVQKLPSFAVSGEE 182
Qy 171 LLLPLFAQAANHLFSIRDVLNADWGISATLRTYQNLKNTYTESNYCINTYQTA 230
Db 183 VPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYDHCVKWYSTG 242
Qy 231 FRGL-NTRLHML---BFTYMFNLVFEYVSIWLFKYQSLV--VSSGANL-----VASGS 280
Db 243 LNNLRGTNAESWRYNQFRKDMTAMVLDLVALFP--SYDTLVVPIKTTTSQLTREVTDAI 300
Qy 281 GP--QQTQSFTSQDW-----PFL-----YSLFQVNSN--YVLNGF 311
Db 301 GTVHPNASFATWYNNNAPSFTIESAVVRNPHLLDLEQVTIYSLLSKWSNTQYNNMW 360
Qy 312 SGARLTQTFPNIQGLPGTTT 331
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Db 361 GGHL--EFRTIGGMLTST 378

RESULT 14

A:Accession: A41052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1181 <LEE>
A:Cross-references: GB:M65252; NID:g142874; PIDN:AAA22410.1; PID:g142875
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 8.4%; Score 277; DB 2; Length 1181;
Best Local Similarity 22.3%; Pred. No. 1.2e-10;
Matches 159; Conservative 106; Mismatches 252; Indels 196; Gaps 33;

QY 6 NNGRTTICDAYNVVAHDPSFEHKS LDTIRKEWMEKRT--DHSLYVAPIVGTVSSFLK 63
DB 3 NNPINEICIPYNCLS-----NPEVVLGGERIETGYTPIDISL-----SLTQFLLS 48
QY 64 K----VGLIGKRLSELGLIPFGSTNLMDILRETEQFLNQLNRLTDTTLARVNAELEG 119
DB 49 EFVPGAGFVLG--LIDLWGFVGPS-----QWDAFLVQIEQLISQRIEFARNQALSRL 102
QY 120 LQANI-----REFNOQVDNPLNTPNPVLSITSSVNTMQQLFLNRLPQFRVQYQL 171
DB 103 L-SNLYQIYAEAFREWE-----ADPTNPALREEMRIQFNDMNSALTITAIPLFTVQNYQV 155
QY 172 LLLPLFAQAANHLFSIRDVLNADWGISATLRTYQNYLKNYTTESYNCINYQTAF 231
DB 156 PLLSVYVQAANHLVSLRDSVFGQWGLDVATINSRYNDLTRIGTYTDYAVRWYNTGL 215
QY 232 R---GLNTRLHDML--EFRTYMFNLNFEYVSWLSFKYQSLVSSGANLYASGGPOOT 285
DB 216 ERVWGPDSR--DWRYNQFRRELTLTVLDIVSLFP-----NYDSRYPIRT 259
QY 286 QSFTSQDWPFLLYSLFQVNSVYLVNGFSGA-----RLTQTF--PNIGGLPGTTT----- 332
DB 260 VSQLTR-----EIVTNPVLENFNGDSFRGSAQRIEQSIRSPHMLDILNSITTYTDAH 310
QY 333 -----HALLAARNVYSGVSS-----GDIGAVFNQ-----NFSCTFLDPL 368
DB 311 GGYVWSGHQIMASPVGSGPEFTPLPYGTWGNAPQQRIVAQGGQGYRTLSSTF--Y 367
QY 369 LTPFVRSWLDGSDRGVNTVNMOTESFESTLGRCAFTARGNSVFPDYFIR----- 423
DB 368 RNPFI-----GIN-----NORLSVLDGTEFAYGSSNLPASVTRKSTV 407
QY 424 -NISGVPLVRNEDLR-----RPLHYNIRIESPSGTPGGLRAYMVSVHNRK-----NNIY 474
DB 408 DLSLDIIPPQDNVPPRQGFSHRLSHVSMFRSGFNSV-SIIRAPMFSWIHRSAEFNII 466
QY 475 AVHE-----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDS 521
DB 467 PSSQITQPLTKSTNLGSGTSVVKGP-----GFT-----GGDI 499
QY 522 LRFEOSTTARTYLRGN-----GNSYNLYLRVSSLGSTIRVTINGRVYVYASNVNTTN 576
DB 500 LR--RTSPQISTLRVITAPLSQRYRVRIRYASTTNLFHTSIDGRPNQGNFSATMSS 557
QY 577 DGVDNNGARFLDINMGVNSDNTNVPLDINV--TNSGTQFELMIMFVPTNL 628
DB 558 GGNLQSGS--FRVGTPTPFNFSNGSSVFTLSAHVNSGVNEVIDRIEFVPAEV 609

RESULT 15

JC2219
parasporal crystal protein cryIAa - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C:Accession: JC2219
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
Biosci. Biotechnol. Biochem. 58, 830-835, 1994
A:Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an
A:Reference number: JC2219; MUID:94289859; PMID:7764972
A:Accession: JC2219
A:Molecule type: DNA
A:Residues: 1-1176 <UDA>
A:Cross-references: DDBJ:D17518; NID:g506190; PIDN:BAA04468.1; PID:g535781
C:Genetics:
A:Gene: cryIA(a)
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 8.3%; Score 276.5; DB 2; Length 1176;
Best Local Similarity 21.5%; Pred. No. 1.3e-10;
Matches 151; Conservative 105; Mismatches 272; Indels 173; Gaps 29;

QY 6 NNGRTTICDAYNVVAHDPSFEHKS LDTIRKEWMEKRT--DHSLYVAPIVGTVSSFLK 63
DB 3 NNPINEICIPYNCLS-----NPEVVLGGERIETGYTPIDISL-----SLTQFLLS 48
QY 64 K----VGLIGKRLSELGLIPFGSTNLMDILRETEQFLNQLNRLTDTTLARVNAELEG 119
DB 49 EFVPGAGFVLG--LVDLIWGFGPS-----QWDAFLVQIEQLINQRIEFARNQALSRL 102
QY 120 LQ-----ANIREFOQVDNPLNTPNPVLSITSSVNTMQQLFLNRLPQFRVQYQL 172
DB 103 LSNLYQIYAEAFREWE-----ADPTNPALREEMRIQFNDMNSALTITAIPLAVQNYQV 156
QY 173 LLLPLFAQAANHLFSIRDVLNADWGISATLRTYQNYLKNYTTESYNCINYQTAF 232
DB 157 LLSVYVQAANHLVSLRDSVFGQWGLDVATINSRYNDLTRIGTYTDYAVRWYNTGL 216
QY 233 ---GLNTRLHDML--EFRTYMFNLNFEYVSWLSFKYQSLVSSGANLYASGGPOOT 286
DB 217 RVWGPDSR--DWRYNQFRRELTLTVLDIVALFS-----NYDSRYPIRTV 260
QY 287 SFTSQDWPFLLYSLFQVNSVYLVNGFSGA-----RLTQTF--PNIGGLPGTTTHALLAA 338
DB 261 SQLTR-----EIVTNPVLENFNGDSFRGSAQRIEQNIRQPHMLDILNSITTYDVHR 311
QY 339 RVNYSGG--VSSGDIGAVFNQFSCSTF-----LPLLT----- 371
DB 312 GFNYWSGHQITASPVG-----FSGPEFAPFLFGNAGNAAPPVLVSLTGLGIFRTLSPL 365
QY 372 FVRSWLDGSDRGVNTVNMOTESFESTLGRCAFTARGNSVFPDYFIRNISGVPLV 431
DB 366 YRRILLGSGNNQELFVLDGTEFSFASLTNLPSTIYRQGT-----VDSLVDIPPQ 417
QY 432 VRNEDLRRLPHY--NEIRNIESPSGTPGGLRAYMVSVHNRK-----NNIYAVHE----- 478
DB 418 DNSVPPRAGFSHRLSHVSMFRSGFNSV-SIIRAPMFSWIHRSAEFNIIPTK 477
QY 479 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDSLRPEQNTTARY 533
DB 478 STNLGSGTSVVKGP-----GFT-----GGDILR--RTSPQIS 508
QY 534 TLRGN-----GNSYNLYLRVSSLGSTIRVTINGRVYVYASNVNTTNNDNGARFLD 588
DB 509 TLRVITAPLSQRYRVRIRYASTTNLFHTSIDGRPNQGNFSATMSS--GSNLQSGSERT 567
QY 589 INMGVNSDNTNVPLDINV--TNSGTQFELMIMFVPTNL 628
DB 568 VGFTTPEFNFSNGSSVFTLSAHVNSGVNEVIDRIEFVPAEV 608

Sat Dec 16:14:54 2003

Search completed: December 12, 2003, 16:18:10
Job time : 23 secs

us-10-040 a-2.rpr

Page 9

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 16:16:21 ; Search time 36 Seconds
(without alignments)

3265.046 Million cell updates/sec

Title: US-10-040-906A-2

Perfect score: 3314

Sequence: 1 MNNVLNNGRTTICDAYNVVA.....GTQELMNVIMFVPTNLPIY 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.pap.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb.pap.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdb.pap.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdb.pap.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.pap.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pdb.pap.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pdb.pap.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pdb.pap.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb.pap.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pdb.pap.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pdb.pap.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pdb.pap.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.pap.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.pap.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3314	100.0	632	12	US-10-040-906A-2
2	3309	99.8	632	12	US-10-040-906A-8
3	3120	94.1	632	12	US-10-040-906A-4
4	3043.5	91.8	634	12	US-10-198-478-12
5	3043.5	91.8	634	12	US-10-102-469-18
6	3010.5	90.8	633	12	US-10-198-478-18
7	3005.5	90.7	634	12	US-10-198-478-2
8	2523.5	76.1	627	12	US-10-040-906A-6
9	311.5	9.4	1156	15	US-10-099-285-72
10	305.5	9.2	643	9	US-09-826-660-25
11	305.5	9.2	1186	9	US-09-826-660-23
12	282.5	8.5	609	12	US-10-107-581-8
13	280.5	8.5	609	12	US-10-107-581-7
14	276.5	8.3	609	12	US-10-107-581-5
15	276.5	8.3	609	12	US-10-107-581-6

16	275.5	8.3	1207	11	US-09-988-462-7	Sequence 7, Appli
17	272	8.2	1177	15	US-10-035-060-6	Sequence 6, Appli
18	271.5	8.2	609	12	US-10-107-581-3	Sequence 3, Appli
19	271.5	8.2	609	12	US-10-107-581-4	Sequence 4, Appli
20	269.5	8.1	667	12	US-10-414-637-8	Sequence 8, Appli
21	269.5	8.1	667	14	US-10-032-717-8	Sequence 8, Appli
22	269.5	8.1	673	12	US-10-414-637-18	Sequence 18, Appli
23	269.5	8.1	673	14	US-10-032-717-18	Sequence 18, Appli
24	269.5	8.1	1210	14	US-10-414-637-4	Sequence 4, Appli
25	269.5	8.1	1210	14	US-10-032-717-4	Sequence 4, Appli
26	268	8.1	615	12	US-10-102-469-8	Sequence 8, Appli
27	268	8.1	617	12	US-10-137-682A-1	Sequence 1, Appli
28	268	8.1	1155	9	US-09-756-643-2	Sequence 2, Appli
29	268	8.1	1155	11	US-09-988-462-9	Sequence 9, Appli
30	268	8.1	1177	12	US-10-102-469-24	Sequence 24, Appli
31	268	8.1	1181	11	US-09-988-462-11	Sequence 11, Appli
32	268	8.1	1181	11	US-09-988-462-13	Sequence 13, Appli
33	268	8.1	1181	11	US-09-988-462-15	Sequence 15, Appli
34	268	8.1	1181	11	US-09-988-462-17	Sequence 17, Appli
35	268	8.1	1181	11	US-09-988-462-28	Sequence 28, Appli
36	267.5	8.1	1178	9	US-09-851-194-2	Sequence 2, Appli
37	266.5	8.0	1178	12	US-10-102-469-10	Sequence 10, Appli
38	266.5	8.0	1178	12	US-10-102-469-12	Sequence 12, Appli
39	266.5	8.0	1178	12	US-10-102-469-14	Sequence 14, Appli
40	266	8.0	1177	15	US-10-035-060-2	Sequence 2, Appli
41	265	8.0	605	9	US-09-826-660-4	Sequence 4, Appli
42	265	8.0	1148	9	US-09-826-660-2	Sequence 2, Appli
43	265	8.0	1174	9	US-09-826-660-6	Sequence 6, Appli
44	265	8.0	1177	9	US-09-873-873-34	Sequence 34, Appli
45	265	8.0	1177	12	US-10-365-645-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1

US-10-040-906A-2
; Sequence 2, Application US/10040906A
; Publication No. US20030167517A1
; GENERAL INFORMATION:
; APPLICANT: Arnaud, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Van Houdt, Sara
; TITLE OF INVENTION: No. US20030167517A1 Bacillus thuringiensis insecticidal protein
; FILE REFERENCE: 58764.000036
; CURRENT APPLICATION NUMBER: US/10/040, 906A
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-040-906A-2

Query Match	100.0%;	Score	3314;	DB	12;	Length	632;
Best Local Similarity	100.0%;	Pred. No.	1.4e-293;	Mismatches	0;	Indels	0;
Matches	632;	Conservative	0;				
Qy	1	MNNVLNNGRTTICDAYNVVAHDPSPFHKSLDITRKEMWEMKRTDHSLYVAPIVGTVSSF	60				
Db	1	MNNVLNNGRTTICDAYNVVAHDPSPFHKSLDITRKEMWEMKRTDHSLYVAPIVGTVSSF	60				
Qy	61	LLKKVGLIGKRLISELWGLIFPSGSGNLNMODILRETEQFLNQLNLTDTLARVNAEGL	120				
Db	61	LLKKVGLIGKRLISELWGLIFPSGSGNLNMODILRETEQFLNQLNLTDTLARVNAEGL	120				
Qy	121	QANIRENQVDNPLNPTONPVLSITSSVNTWQOLFNLRLPQPRVQGYQLLLPLPAQA	180				
Db	121	QANIRENQVDNPLNPTONPVLSITSSVNTWQOLFNLRLPQPRVQGYQLLLPLPAQA	180				

QY 181 ANMHLSPFRDVLNADWGI SAATLRTYQNYLKNYTTESYNYCINTYQTAFGLNTRLHD 240
DB 181 ANMHLSPFRDVLNADWGI SAATLRTYQNYLKNYTTESYNYCINTYQTAFGLNTRLHD 240
QY 241 MLEPRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQQTQSFTSDWPFYLSLF 300
DB 241 MLEPRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQQTQSFTSDWPFYLSLF 300
QY 301 QVNSYVLNGFSGARLTOTFPNIGGLPGTTTTTHALLAARVNYSGVSSGDI GAVFNQNF 360
DB 301 QVNSYVLNGFSGARLTOTFPNIGGLPGTTTTTHALLAARVNYSGVSSGDI GAVFNQNF 360
QY 361 CSTFLPPLLTTPFVRSWLDGSGDRGVNTVWQTESFESTLGLRCGAFARGNSNYPPDY 420
DB 361 CSTFLPPLLTTPFVRSWLDGSGDRGVNTVWQTESFESTLGLRCGAFARGNSNYPPDY 420
QY 421 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
DB 421 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
QY 481 TMIHLAPEDYTGFTTISPITHATQVNNQTRTFISEKFGNQDSLRFEQSNTTARYTLRGNGN 540
DB 481 TMIHLAPEDYTGFTTISPITHATQVNNQTRTFISEKFGNQDSLRFEQSNTTARYTLRGNGN 540
QY 541 SYNLYRVSSLGNSITRTVINGRVVYTSANVNTTNNDCVNDGNGARFLDINNMGVVASDNT 600
DB 541 SYNLYRVSSLGNSITRTVINGRVVYTSANVNTTNNDCVNDGNGARFLDINNMGVVASDNT 600
QY 601 NVPLDINTFNSGTQFELMNMIFVPTNLPPIY 632
DB 601 NVPLDINTFNSGTQFELMNMIFVPTNLPPIY 632

RESULT 2

US-10-040-906A-8
; Sequence 8, Application US/10040906A
; Publication No. US20030167517A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Van Houdt, Sara
; TITLE OF INVENTION: No. US20030167517A1el Bacillus thuringiensis insecticidal protein
; FILE REFERENCE: 58764.000036
; CURRENT APPLICATION NUMBER: US/10/040.906A
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Artificial Sequence
US-10-040-906A-8

Query Match 99.8%; Score 3309; DB 12; Length 633;
Best Local Similarity 100.0%; Pred. No. 4e-293;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNVLNNGRTTICDAYNVVAHDPPFSEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSFL 61
DB 3 NNVLNNGRTTICDAYNVVAHDPPFSEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSFL 62
QY 62 LKKVGSILGKRLSELWGLIFPSSGNTLMQDILRETEQFLNQRNTDTTLARVNAELGLQ 121
DB 63 LKKVGSILGKRLSELWGLIFPSSGNTLMQDILRETEQFLNQRNTDTTLARVNAELGLQ 122
QY 122 ANIREFNOQVDNPLNPTNPVLSITSSVNTWQQLFLNRLPQFRVQGYQLLLPLFAQA 181
DB 123 ANIREFNOQVDNPLNPTNPVLSITSSVNTWQQLFLNRLPQFRVQGYQLLLPLFAQA 182

QY 182 NMHLSPFRDVLNADWGI SAATLRTYQNYLKNYTTESYNYCINTYQTAFGLNTRLHD 241
DB 182 NMHLSPFRDVLNADWGI SAATLRTYQNYLKNYTTESYNYCINTYQTAFGLNTRLHD 242
QY 242 MLEPRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQQTQSFTSDWPFYLSLF 301
DB 242 MLEPRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQQTQSFTSDWPFYLSLF 302
QY 302 VNSYVLNGFSGARLTOTFPNIGGLPGTTTTTHALLAARVNYSGVSSGDI GAVFNQNF 361
DB 302 VNSYVLNGFSGARLTOTFPNIGGLPGTTTTTHALLAARVNYSGVSSGDI GAVFNQNF 362
QY 362 STFLPPLLTTPFVRSWLDGSGDRGVNTVWQTESFESTLGLRCGAFARGNSNYPPDY 421
DB 362 STFLPPLLTTPFVRSWLDGSGDRGVNTVWQTESFESTLGLRCGAFARGNSNYPPDY 422
QY 422 IRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 481
DB 422 IRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 482
QY 482 MLEPRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQQTQSFTSDWPFYLSLF 541
DB 482 MLEPRTYMLNVEFVYSIWSLFKYQSLVSSGANLYASGSGPQQQTQSFTSDWPFYLSLF 542
QY 542 SYNLYRVSSLGNSITRTVINGRVVYTSANVNTTNNDCVNDGNGARFLDINNMGVVASDNT 601
DB 542 SYNLYRVSSLGNSITRTVINGRVVYTSANVNTTNNDCVNDGNGARFLDINNMGVVASDNT 602
QY 602 NVPLDINTFNSGTQFELMNMIFVPTNLPPIY 632
DB 602 NVPLDINTFNSGTQFELMNMIFVPTNLPPIY 633

RESULT 3

US-10-040-906A-4
; Sequence 4, Application US/10040906A
; Publication No. US20030167517A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Van Houdt, Sara
; TITLE OF INVENTION: No. US20030167517A1el Bacillus thuringiensis insecticidal protein
; FILE REFERENCE: 58764.000036
; CURRENT APPLICATION NUMBER: US/10/040.906A
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-040-906A-4

Query Match 94.1%; Score 3120; DB 12; Length 632;
Best Local Similarity 93.4%; Pred. No. 7.2e-276;
Matches 590; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 1 MNVLNNGRTTICDAYNVVAHDPPFSEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSFL 60
DB 1 MNSVLNNGRTTICDAYNVVAHDPPFSEHKSLDTIRKEWMEWKRTDHSLYVAPIVGTVSSFL 60
QY 61 LKKVGSILGKRLSELWGLIFPSSGNTLMQDILRETEQFLNQRNTDTTLARVNAELGL 120
DB 61 LKKVGSILGKRLSELWGLIFPSSGNTLMQDILRETEQFLNQRNTDTTLARVNAELGL 120
QY 121 ANIREFNOQVDNPLNPTNPVLSITSSVNTWQQLFLNRLPQFRVQGYQLLLPLFAQA 180
DB 121 ANIREFNOQVDNPLNPTNPVLSITSSVNTWQQLFLNRLPQFRVQGYQLLLPLFAQA 180
QY 181 ANMHLSPFRDVLNADWGI SAATLRTYQNYLKNYTTESYNYCINTYQTAFGLNTRLHD 240

Db 181 ANLHLSFIRDVLNADENGISAATLRTYQNHRLNRYTRDYSNYCINTYQTAFRGLNRLHD 240
Qy 241 MLEFRTYMLNVEYVSIWSLKYQSLVSSGANLYASGSGPQQTQSPTSDWPFYSLF 300
Db 241 MLEFRTYMLNVEYVSIWSLKYQSLVSSGANLYASGSGPQQTQSPTSDWPFYSLF 300
Qy 301 QVNSNYVLNGSGARLTOTFPNIGLPGTTTTTHALLAARVNYSGVSSGDI GAVENQNF 360
Db 301 QVNSNYVLNGSGARLTOTFPNIGLPGTTTTTHALLAARVNYSGVSSGDI GAVENQNF 360
Qy 361 CSTFLPPLLTTPVRSLWDSGDRGVNTVNNQTESFSTGLRCGATFARGNSNYFPDY 420
Db 361 CSTFLPPLLTTPVRSLWDSGDRGVNTVNNQTESFSTGLRCGATFARGNSNYFPDY 420
Qy 421 FIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 421 FIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Qy 481 TMIHLAPEDYTGFTTSPHATQVNNQTRTFISEKEFGNQGDSLRPFQSNNTTARYTLRGNGN 540
Db 481 TMIHLAPEDYTGFTTSPHATQVNNQTRTFISEKEFGNQGDSLRPFQSNNTTARYTLRGNGN 540
Qy 541 SYNLYRVSSLSGNSIRVTINGRVTASNVNTTNNQVNDNGARFLDINNMGNNVASDNT 600
Db 541 SYNLYRVSSLSGNSIRVTINGRVTASNVNTTNNQVNDNGARFLDINNMGNNVASDNT 600
Qy 601 NVPLDINTVNSGTQFELMNMIFVPTNLPIY 632
Db 601 NVPLDINTVNSGTQFELMNMIFVPTNLPIY 632

RESULT 4
US-10-198-478-12
; Sequence 12, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 634
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: an amino acid sequence encoded by a completely synthesized nucleotide sequence

Query Match 91.8%; Score 3043.5; DB 12; Length 634;
Best Local Similarity 90.7%; Pred. No. 7e-269;
Matches 573; Conservative 34; Mismatches 24; Indels 1; Gaps 1;
Qy 2 NVNLNNGRTTICDANVVAHDPPFSEKSLDTIRKEMWEKRTDHSLYVAPVGVTSFSL 61
Db 3 NVNLNNGRTTICDANVVAHDPPFSEKSLDTIRKEMWEKRTDHSLYVAPVGVTSFSL 62
Qy 62 LKKGSLIGKRLSELWGLIFPSGSLNMQDLIRETEQFLNQLRTDTLARVNAEGLQ 121
Db 63 LKKGSLIGKRLSELWGLIFPSGSLNMQDLIRETEQFLNQLRTDTLARVNAEGLQ 122
Qy 122 ANIREFNOQVDNLTQNPVPLSITSSVNTMQQLFLNRLPQFOIQGVQLLLPLFAQA 181

Db 123 ANIREFNOQVDNLTQNPVPLSITSSVNTMQQLFLNRLPQFOIQGVQLLLPLFAQA 182
Qy 182 NMHLSFIRDVLNADENGISAATLRTYQNHRLNRYTRDYSNYCINTYQTAFRGLNRLHD 241
Db 183 NMHLSFIRDVLNADENGISAATLRTYQNHRLNRYTRDYSNYCINTYQTAFRGLNRLHD 242
Qy 242 LEPTYMFLNVEYVSIWSLKYQSLVSSGANLYASGSGPQQTQSPTSDWPFYSLF 301
Db 243 LEPTYMFLNVEYVSIWSLKYQSLVSSGANLYASGSGPQQTQSPTSDWPFYSLF 302
Qy 302 VNSNYVLNGSGARLTOTFPNIGLPGTTTTTHALLAARVNYSGVSSGDI GAVENQNF 360
Db 303 VNSNYVLNGSGARLTOTFPNIGLPGTTTTTHALLAARVNYSGVSSGDI GAVENQNF 362
Qy 361 CSTFLPPLLTTPVRSLWDSGDRGVNTVNNQTESFSTGLRCGATFARGNSNYFPDY 420
Db 363 CSTFLPPLLTTPVRSLWDSGDRGVNTVNNQTESFSTGLRCGATFARGNSNYFPDY 422
Qy 421 FIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 423 FIRNIGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 482
Qy 481 TMIHLAPEDYTGFTTSPHATQVNNQTRTFISEKEFGNQGDSLRPFQSNNTTARYTLRGNGN 540
Db 483 TMIHLAPEDYTGFTTSPHATQVNNQTRTFISEKEFGNQGDSLRPFQSNNTTARYTLRGNGN 542
Qy 541 SYNLYRVSSLSGNSIRVTINGRVTASNVNTTNNQVNDNGARFLDINNMGNNVASDNT 600
Db 543 SYNLYRVSSLSGNSIRVTINGRVTASNVNTTNNQVNDNGARFLDINNMGNNVASDNT 602
Qy 601 NVPLDINTVNSGTQFELMNMIFVPTNLPIY 632
Db 603 NVPLDINTVNSGTQFELMNMIFVPTNLPIY 634

RESULT 5
US-10-102-469-18
; Sequence 18, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; APPLICANT: Perlak, Frederick J.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT APPLICATION NUMBER: US/10/102,469
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 634
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic structural gene encoding P2 insecticidal protein

Query Match 91.8%; Score 3043.5; DB 12; Length 634;
Best Local Similarity 90.7%; Pred. No. 7e-269;
Matches 573; Conservative 34; Mismatches 24; Indels 1; Gaps 1;
Qy 2 NVNLNNGRTTICDANVVAHDPPFSEKSLDTIRKEMWEKRTDHSLYVAPVGVTSFSL 61
Db 3 NVNLNNGRTTICDANVVAHDPPFSEKSLDTIRKEMWEKRTDHSLYVAPVGVTSFSL 62
Qy 62 LKKGSLIGKRLSELWGLIFPSGSLNMQDLIRETEQFLNQLRTDTLARVNAEGLQ 121

Db 63 LKVGSLGKRLSELWGLIFSGSTNLMDILRETEQFLNRLNDTLARVNAELIGLQ 122
QY 122 ANIREFNOQVDNPLNPTQNPVLSITSSVNTWQOLFLNRLPQFRVQGYQLLLPLFAQAA 181
Db 123 ANIREFNOQVDNPLNPTQNPVLSITSSVNTWQOLFLNRLPQFRVQGYQLLLPLFAQAA 182
QY 182 NMHLSFIRDVLNADWEGISAATLRTYQNYLKNYTTSEYSCINCYQTAFLGNLRLHDM 241
Db 183 NMHLSFIRDVLNADWEGISAATLRTYQNYLKNYTTSEYSCINCYQTAFLGNLRLHDM 242
QY 242 LEFRYTMFLNVEYVSIWLSFKYQSLVSSGANLYASGGPQOQTSQDWPFLYSLFQ 301
Db 243 LEFRYTMFLNVEYVSIWLSFKYQSLVSSGANLYASGGPQOQTSQDWPFLYSLFQ 302
QY 302 VNSNYVLNGFSGARLTQTPNPNGIGLPGTTTHALLAARVNSYGGVSSGGDGA- FNONFS 360
Db 303 VNSNYVLNGFSGARLTQTPNPNGIGLPGTTTHALLAARVNSYGGVSSGGDGA- FNONFS 362
QY 361 CSTFLPPLLTTPVRSWLDGSDRGVNTVNMWQTESFESTLGLRCGAFTARGNSYFPDY 420
Db 363 CSTFLPPLLTTPVRSWLDGSDRGVNTVNMWQTESFESTLGLRCGAFTARGNSYFPDY 422
QY 421 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
Db 423 FIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 482
QY 481 TMIHLAPEDYTGFTISPIHATOVNQTTFISEKFGNOGDSLRFESQNTTARYTLRGNG 540
Db 483 TMIHLAPEDYTGFTISPIHATOVNQTTFISEKFGNOGDSLRFESQNTTARYTLRGNG 542
QY 541 SYNLVLRVSSLSGNSIRTVINGRVYTVASVNTTNDGVNDNGARFLDINMGNVASDN 600
Db 543 SYNLVLRVSSLSGNSIRTVINGRVYTVASVNTTNDGVNDNGARFLDINMGNVASDN 602
QY 601 NVPLDINTVNSGTOFELNMIMFVPTNLPPY 632
Db 603 NVPLDINTVNSGTOFELNMIMFVPTNLPPY 634

RESULT 6
US-10-198-478-18
; Sequence 18, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198, 478
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-198-478-18

Query Match 90.8%; Score 3010.5; DB 12; Length 633;
Best Local Similarity 89.7%; Pred. No. 7.2e-266;
Matches 568; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

QY 1 MNNVLNNGRTTICDAYNVVAHDPPSFSEHKSLDITIRKEMWKRTHDLSLYVAPIVGTVSSSF 60
Db 1 MNSVLNNGRTTICDAYNVVAHDPPSFSEHKSLDITIRKEMWKRTHDLSLYVAPIVGTVSSSF 60
QY 61 LLKKVGSILGKRLSELWGLIFSGSTNLMDILRETEQFLNRLNDTLARVNAELIGL 120
Db 61 LLKKVGSILGKRLSELWGLIFSGSTNLMDILRETEQFLNRLNDTLARVNAELIGL 120

QY 121 QANIREFNOQVDNPLNPTQNPVLSITSSVNTWQOLFLNRLPQFRVQGYQLLLPLFAQA 180
Db 121 QANVEEFNRQVDNPLNPNRAVPLSITSSVNTWQOLFLNRLPQFRVQGYQLLLPLFAQA 180
QY 181 ANMHLSTFRDVLNADWEGISAATLRTYQNYLKNYTTSEYSCINCYQTAFLGNLRLHDM 240
Db 181 ANMHLSTFRDVLNADWEGISAATLRTYQNYLKNYTTSEYSCINCYQTAFLGNLRLHDM 240
QY 241 MLEPRTYTMFLNVEYVSIWLSFKYQSLVSSGANLYASGGPQOQTSQDWPFLYSLF 300
Db 241 MLEPRTYTMFLNVEYVSIWLSFKYQSLVSSGANLYASGGPQOQTSQDWPFLYSLF 300
QY 301 QVNSNYVLNGFSGARLTQTPNPNGIGLPGTTTHALLAARVNSYGGVSSGGDGA- FVFNQNF 359
Db 301 QVNSNYVLNGFSGARLTQTPNPNGIGLPGTTTHALLAARVNSYGGVSSGGDGA- FVFNQNF 360
QY 360 SCSTFLPPLLTTPVRSWLDGSDRGVNTVNMWQTESFESTLGLRCGAFTARGNSYFPD 419
Db 361 NCSTFLPPLLTTPVRSWLDGSDRGVNTVNMWQTESFESTLGLRCGAFTARGNSYFPD 420
QY 420 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 479
Db 421 YFIRNISGVPLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVHNRKNNIYAVHENG 480
QY 480 GTMIHLAPEDYTGFTISPIHATOVNQTTFISEKFGNOGDSLRFESQNTTARYTLRGNG 539
Db 481 GTMIHLAPEDYTGFTISPIHATOVNQTTFISEKFGNOGDSLRFESQNTTARYTLRGNG 540
QY 540 NSYNLYRVSSLSGNSIRTVINGRVYTVASVNTTNDGVNDNGARFLDINMGNVASDN 599
Db 541 NSYNLYRVSSLSGNSIRTVINGRVYTVASVNTTNDGVNDNGARFLDINMGNVASDN 600
QY 600 TNVPLDINTVNSGTOFELNMIMFVPTNLPPY 632
Db 601 SDVPLDINTVNSGTOFELNMIMFVPTNLPPY 633

RESULT 7

US-10-198-478-2
; Sequence 2, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:

; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198, 478
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 634
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: an amino acid sequence encoded by a completely synthesized nucleotide
; OTHER INFORMATION: tide sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(634)
; OTHER INFORMATION:
US-10-198-478-2

Query Match 90.7%; Score 3005.5; DB 12; Length 634;
Best Local Similarity 89.7%; Pred. No. 2.1e-265;
Matches 567; Conservative 39; Mismatches 25; Indels 1; Gaps 1;

QY 2 NNVVLNNGRTTICDAYNVVAHDPPSFSEHKSLDITIRKEMWKRTHDLSLYVAPIVGTVSSFL 61
Db 3 NSVLNNGRTTICDAYNVVAHDPPSFSEHKSLDITIRKEMWKRTHDLSLYVAPIVGTVSSFL 62

Qy 62 LKKGSLIGKRLSELWGLIPPSGSLNMODILRETEQFLNORLNTDTLARNVAELSLQ 121
Db 63 LKKGSLVGRKRLSELNRLIPPSGSLNMODILRETEKFLNORLNTDTLARNVAELSLQ 122
Qy 122 ANIREFNOQVDNPLNPTQNPVPLSITSSVNTMOQLFLNRLPQFRVQVQQLLLPLFAQA 181
Db 123 ANVEEFNRQVDNPLNPNRNPVPLSITSSVNTMOQLFLNRLPQFQVQVQQLLLPLFAQA 182
Qy 182 NMHLSFIRDVNLNADWGISAATLRTYQNYLKNYTYEYNYCINTYQTAFLNRLHDM 241
Db 183 NLHLSFIRDVNLNADWGISAATLRTYQNYLKNYTYEYNYCINTYQTAFLNRLHDM 242
Qy 242 LEPTFMFLNVEFVYSIWSLKYQSLVSSGANLYASGSGPQOQTSODWPELYSLFQ 301
Db 243 LEPTFMFLNVEFVYSIWSLKYQSLVSSGANLYASGSGPQOQTSODWPELYSLFQ 302
Qy 302 VNSNYLVNGFSGARLTOTFPNIGLPGTTTTTHALLAARVNSGVSGDIGA - VFNQVFS 360
Db 303 VNSNYLVNGFSGARLNTFPNIGLPGTTTTTHALLAARVNSGVSGDIGA - VFNQVFS 362
Qy 361 CSTPLPPLLTFFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYPDY 420
Db 363 CSTPLPPLLTFFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNYPDY 422
Qy 421 FIRMISGVLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVNRRKNIYAVHENG 480
Db 423 FIRMISGVLVVRNEDLRPLHYNEIRNIESPSGTPGGLRAYMVSVNRRKNIYAVHENG 482
Qy 481 TMIHLAPEDYTGFISPIHATQVNNQTRTFISEKFGQDLSRFEQNTTARYTLRGNGN 540
Db 483 SMHHLANDYTGFISPIHATQVNNQTRTFISEKFGQDLSRFEQNTTARYTLRGNGN 542
Qy 541 SYNLVLRVSSIGNSTIRVINGRVTASNVNTTNDGVNDNGARFLDINMGNVASDNT 600
Db 543 SYNLVLRVSSIGNSTIRVINGRVTATVNTTNDGVNDNGARFSDINIGNVASSNS 602
Qy 601 NVPLDINTVNSGTQFELNMIMFVPTNLPIY 632
Db 603 DVPLDINTVNSGTQFELNMIMFVPTNLPIY 634

RESULT 8
US-10-040-906A-6
; Sequence 6, Application US/10040906A
; Publication No. US20030167517A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Van Houdt, Sara
; TITLE OF INVENTION: No. US20030167517A1 Bacillus thuringiensis insecticidal protein
; FILE REFERENCE: 58764.000036
; CURRENT APPLICATION NUMBER: US/10/040.906A
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 6
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-040-906A-6

Query Match 76.1%; Score 2523.5; DB 12; Length 627;
Best Local Similarity 77.5%; Pred. No. 2.1e-221;
Matches 495; Conservative 42; Mismatches 83; Indels 19; Gaps 7;

Qy 1 MNNVLNNGRTTICDAYNVVAHDPFSFEHKSJDTIRKEMWEMKRTDHSILYVAPIVGTVSSF 60
Db 1 MNNVLNNGRTTICDAYNVVAHDPFSFEHKSJDTIRKEMWEMKRTDHSILYVAPIVGTVSSF 60
Qy 61 LKKGSLIGKRLSELWGLIPPSGSLNMODILRETEQFLNORLNTDTLARNVAELSLQ 120
Db 63 LKKGSLVGRKRLSELNRLIPPSGSLNMODILRETEKFLNORLNTDTLARNVAELSLQ 122

Db 61 LKKGSLIGKRLSELKNIILPFGSIESMODILRGAEQFLNORLNTDADTSRVEAEARGL 120
Qy 121 QANIREFNOQVDNPLNPTQNPVPLSITSSVNTMOQLFLNRLPQFRVQVQQLLLPLPAQA 180
Db 121 QANVEEFNRQVDNPLNPNRNPVPLSITSSVNTMOQLFLNRLPQFQVQVQQLLLPLPAQA 180
Qy 181 ANHLSFIRDVNLNADWGISAATLRTYQNYLKNYTYEYNYCINTYQTAFLNRLHDM 240
Db 181 ANHLSFIRDVNLNADWGISAATLRTYQNYLKNYTYEYNYCINTYQTAFLNRLHDM 240
Qy 241 MLEFRTYMFNVLNVEFVYSIWSLKYQSLVSSGANLYASGSGPQOQTSODWPELYSLF 300
Db 241 MLEFRTYMFNVLNVEFVYSIWSLKYQSLVSSGANLYASGSGPQOQTSODWPELYSLF 300
Qy 301 QVNSNYLVNGFSGARLTOTFPNIGLPGTTTTTHALLAARVNSGVSGDIGA - VFNQVFS 357
Db 301 QVNSNYLVNGFSGARLTOTFPNIGLPGTTTTTHALLAARVNSGVSGDIGA - VFNQVFS 353
Qy 358 NFSCSTFLPPLLTFFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNY 416
Db 354 NFSCSTFLPPLLTFFVRSWLDSDRGVNTVNTWQTESFESTLGLRCGAFARGNSNY 408
Qy 417 FPDYFIRNISGVLVVRNEDLRPLHYNEIRNIESPSGTP - GGLR - AYVSVNRRKNI 473
Db 409 FPDYFIRNISGVLVVRNEDLRPLHYNEIRNIESPSGTP - GGLR - AYVSVNRRKNI 468
Qy 474 YAVHENGTMHILAPEDYTGFISPIHATQVNNQTRTFISEKFGQDLSRFEQNTTARY 533
Db 469 YAAHENGTMHILAPEDYTGFISPIHATQVNNQTRTFISEKFGQDLSRFEQNTTARY 528
Qy 534 TLRGNGSNLYLRVSSIGNSTIRVINGRVTASNVNTTNDGVNDNGARFLDINMGN 593
Db 529 TLRGNGSNLYLRVSSIGNSTIRVINGRVTASNVNTTNDGVNDNGARFSDINIGN 588
Qy 594 VASDNTVNSGTQFELNMIMFVPTNLPIY 632
Db 589 VASDNTVNSGTQFELNMIMFVPTNLPIY 627

RESULT 9
US-10-099-285-72
; Sequence 72, Application US/10099285
; Publication No. US20030105319A1
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099.285
; FILING DATE: 15-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/002.285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886.615
; FILING DATE: 1-JUL-1997

RESULT 10

Db 610 SGSQT---AGISISNAGRTQPHFDKIEFIP 637

RESULT 11

US-09-826-660-23

Sequence 23, Application US/09826660

Patent No. US20010026940A1

GENERAL INFORMATION:

APPLICANT: Cardineau, Guy A.

APPLICANT: Stelman, Steven J.

APPLICANT: Narva, Kenneth E.

TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

FILE REFERENCE: MA-714XC2D1

CURRENT APPLICATION NUMBER: US/09/826,660

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 09/178,252

PRIOR FILING DATE: 1998-10-23

PRIOR APPLICATION NUMBER: 60/065,215

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/076,445

PRIOR FILING DATE: 1998-03-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 23

LENGTH: 1186

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Toxin encoded by synthetic B.t. gene

US-09-826-660-23

Query Match 9.2%; Score 305.5; DB 9; Length 1186;

Best Local Similarity 22.5%; Pred. No. 2e-18;

Matches 142; Conservative 101; Mismatches 265; Indels 123; Gaps 25;

Qy 52 PIVGVTSFLLKVKGLICKRLSELWGLIPSGSTNLMDILRETEQFLNQLRNTDTLA 111

Db 73 PFAGIASFYSFLVG-----ELW-----PRG-RDPWEIFLEHVEQLIRQQVTEFRD 118

Qy 112 RVNBEGLQANIREFNQOVNFLNPTQNPVPLSTSSVNTMQOL-FLNRLPQFVQGYQ 170

Db 119 TALARLOGLSNFRAYQOSLEDWLENRDDARTSVLYTQYALELDLFLNAPLFAIRNQE 178

Qy 171 LLLPLFAQANHLSPFRDVLNADWGISATLRTYQNYLKNYTTYSNYCINTYOTA 230

Db 179 VPLLMVYQAANLHLLLRDASLFGSEFLTSGEIQRYVERQVETREYSYCARWYNTG 238

Qy 231 FRGL-NTRLHDML---ERTYMLNVPFVYSIWSLFKYQSLVSSGANL-----YASGSP 282

Db 239 LNNLRGTNAESLRYNQFRDRLTLGLDLVALFSPYDTRVYPMNTSAQLTREIYTDPIGR 298

Qy 283 QOTQS-FTSQDWPFYLSLFQVNSNYVLNGFSGARLTQTF-PNIGGLPGTTTHALLAARV 340

Db 299 TNAPSGFASTNW-----FNNN--APSFSAIEAAVIRPPLHLDFFPQLTIFSVLSRWS 348

Qy 341 NYSGVSSGDIQAVFNQNFSCSTFLPLTPFRSW-----LDSGDRGGVNTVTN----- 391

Db 349 N-----TQYMNWVGHRLSRTIRGSLSTSGTNT 380

Qy 392 -----WQTESFES-----TLGLRCGAFARGNSNYFPDFIRNI--SG 427

Db 381 SINPVTLOFTGRDVRTESFAGINILLTTPVNGVPMFARNRPNLNSLRGSLLYTIGYT 440

Qy 428 VPLVRNEDLRPLHYNIRNIESPSGTPGGRAYMVSVVHNRKNNIYA-VHENGTMHLA 486

Db 441 VGTQLFDESELPPTTERPNVESYHRLSNIR--LISGTLRAVYVSWTHRSA----- 492

Qy 487 PEDYTGFTISPIHATQVN-----NQRRTFISEKFGNQSLSRPEQSNNTARYTLRNG 539

Db 493 --DRTN--TISDSITQIPLVKSFLNLSGTSVVSFGPTGGDIIRTNVNGSVLSMGLNFN 549

Qy 540 NS---YNLYLRVSSLGNSITIRTING-RVYASNTNTTNDGNDNGARFLDINMGV 595

Db 550 TSLQRYRVRYAASQTMVLRLVTVGGSTTFDQGPPTMSANESLTSQSPRPAEPVVGISA 609

Qy 596 ASDNTNPLDINTFNSTGTQ-FELNMIMFVP 625

Db 610 SGSQT---AGISISNAGRTQPHFDKIEFIP 637

RESULT 12

US-10-107-581-8

Sequence 8, Application US/10107581

Publication No. US20030188335A1

GENERAL INFORMATION:

APPLICANT: Tull, Rakesh

TITLE OF INVENTION: CHIMERIC & ENDOTOXIN PROTEIN WITH

TITLE OF INVENTION: EXTRAORDINARILY HIGH INSECTICIDAL ACTIVITY

FILE REFERENCE: 07064-014001

CURRENT APPLICATION NUMBER: US/10/107,581

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8

LENGTH: 609

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-107-581-8

Query Match 8.5%; Score 282.5; DB 12; Length 609;

Best Local Similarity 21.7%; Pred. No. 9.1e-17;

Matches 152; Conservative 105; Mismatches 271; Indels 173; Gaps 29;

Qy 6 NNGTTTCDAYNVVAHDPFSEHKSLDTIRKEMWERT--DHSLYVAVIPVGTVSSFLK 63

Db 3 NNPINCEIPYCNLS-----NPEVEVLGRIETGYTPIDISL-----SLTQFLLS 48

Qy 64 K-----VGLICKRLSELWGLIPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELG 119

Db 49 ETVPGAGFVLG--LVDIIMGIFGFS-----QWDAFLVQLQEQINRIEFAFNQAIISRUEG 102

Qy 120 LQ-----ANIREFNQOVNFLNPTQNPVPLSTSSVNTMQOLFLNRLPQFVQGYQLL 172

Db 103 LSNLYQIYAESFREWE-----ADPTNPALREENRIQFNDMNSALTTAIPLFAVQNYQVP 156

Qy 173 LLPLFAQANHLSPFRDVLNADWGISATLRTYQNYLKNYTTYSNYCINTYOTA 232

Db 157 LLSVYQAANLHLLLRDASLFGSEFLTSGEIQRYVERQVETREYSYCARWYNTG 216

Qy 233 ---GLNTRLHDML---ERTYMLNVPFVYSIWSLFKYQSLVSSGANLYASGSPQOTQ 286

Db 217 RVWGPDSR--DWVRYNQFRRELTUTLVDI VALPS-----NYDSRRYPRTV 260

Qy 287 SFTSQDWPFYLSLFQVNSNYVLNGFSGA-----RLTQTF--PNIGGLPGTTTHALLAA 338

Db 261 SOLTR-----EIVTNPVLENFDCGFRGMAQRIEQINRQPHMLDILNSITITVDVHR 311

Qy 339 RVNYSGG--VSSGDIGAVFNQNFSCSTP-----LPPLTTP----- 371

Db 312 GFNYWSGHQITASPVG-----FSGPEFAPPLFGNAGNAAPPVLVSLTGLGIFRTLSSPL 365

Qy 372 FVRSWLDGSDRGVNTVTNMQTESFESTLGRCAFTARGNSNYPDYFIRNISGVPLV 431

Db 366 YRRILGSGNNQBLFVLDGTGFESFASLTNLPSTPIYRQGT-----VDSLDVIPPQ 417

Qy 432 VRNEDLRPLHY--NEIRNIESPSGTPGGRAYMVSVVHNRK--NNIYAVHE----- 478

Db 418 DNSVPPRAGPSHRLSHVTMLSOAGAVYTLRAPTFSSHQHSABENNIIPSSQITQIPLTK 477

Qy 479 ---NGTMHLAPEDYTGFTISPIHATQVNNTQRTFISEKFGNQSLSRPEQSNNTARY 533

Db 478 STNLGSGTSVVKGP---GFT-----GGDILR--RTSPGQIS 508

Qy 534 TLRGN-----GNSNLYLRVSSLGNSITIRTINGRVYASNTNTTNDGNDNGARFLD 588

Db 509 TLRVNTITAPLSQRYRVRYASTTNLQFTSIDGRPINQGNFSATMSS--GSNLOGSGFRT 567

QY	589	INMGENVASDNTNVPLOINV-TFNSCTQPELMNIMFVPTNL	628
	:	:	:
D6	568	VGFTPTTFNSGSSVFTLSAHFVNSGNEVYIDRIEFVPAEV	608
	:	:	:

```

RESULT 13
US-10-107-581-7
; Sequence 7, Application US/10107581
; Publication No. US20030188335A1
; GENERAL INFORMATION:
; APPLICANT: Tuli, Rakesh
; TITLE OF INVENTION: CHIMERIC & ENDOTOXIN PROTEIN WITH
; FILE REFERENCE: 07064-014001
; CURRENT APPLICATION NUMBER: US/10/107,581
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-107-581-7

```

[illegible]

```

Qy 589 INMGNVASONTNVPLDINV-TFNSGTOGFELMNMIFVPTNL 628
      :      :      :      :      :      :      :      :
Db 568 VGFTHPPFNSGSSVFTLSARVFNSGNEVYDRIEFVPAEV 608
      :      :      :      :      :      :      :      :

RESULT 14
US-10-107-581-5
; Sequence 5, Application US/10107581
; Publication No. US20030188335A1
; GENERAL INFORMATION:
; APPLICANT: Tuli, Rakesh
; TITLE OF INVENTION: CHIMERIC & ENDOTOXIN PROTEIN WITH
; TITLE OF INVENTION: EXTRAORDINARILY HIGH INSECTICIDAL ACTIVITY
; FILE REFERENCE: 07064-014001
; CURRENT APPLICATION NUMBER: US/10/107,581
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-10-107-581-5

```

Query Match	8.3%	Score 276.5	DB 12	Length 609
Best Local Similarity	21.5%	Pred. No. 3.2e-16		
Matches 151	Conservative 105	Mismatches 272	Indels 173	Gaps 29
Qy	6	NNGRTTICDANNVVAHDPFSEHKSLDITIRKENWEKRT--DHSLYVAPIVGTVSSFLK	63	
Db	3	NNPNINECIPNCLSS-----NPEVVLGGERIETGYPIDISL-----SUTQFLLS	48	
Qy	64	K-----VGSLGICKRILSELWGLIFPSGSTNLMDILRETEQFLNORLNTDTLARNVAELEG	119	
Db	49	EFPVPGAGFVLG--LVLDIWIIGFPGS---QWDAFLVQIEQLINQRIEFPARNQAIISRLG	102	
Qy	120	LQ-----ANIREFNOQVDNFLNPTQNVPLSITSSVNTWMOQLFLNRLPQFRVQGYQLL	172	
Db	103	LSNLYQIYAESFREWE-----ADPTNPALREEMRIQFNDMNSALTTAIPLLAQNVQVP	156	
Qy	173	LLPLFAQAAHNLSPFRDVLNADENWIGISAAITLTYONYLKNYTEYSNYCINTYQTAFR	232	
Db	157	LLSVYQAAHNLHLSVRDVSFGQRMWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLE	216	
Qy	233	--GLNTRLHMLG--EFRYTMELNVPEYYSIWSLKFYQSVLLVSSGANLYASGGSPQOTQ	286	
Db	217	RWVGPDGR--DWRYNQFRRELTVLVDIIVALFS-----NYDSRRYPIDTV	260	
Qy	287	SFTSQDWPFLYSLFQVNSNTVNLGFGSA-----RLQTQF--PNIGLPGTTTTALLAA	338	
Db	261	SQLTR-----EIVTNPVLENFDGSPRGMARIEQINRQPHLMDILNSITIYTDVHR	311	
Qy	339	RVNYSGG--VSSGDIGAVFNQNSCSTF-----LPPLLT-----	371	
Db	312	GFNYWSHQITASPGV-----FSGPEFAPFLFGNAGNAAPPVLVSLTGLGIFRTLSSPL	365	
Qy	372	FVRSWLDSDGDRGVNVTVMNQWTESPSTGLRCGAFTARGSNVFPDYFIKNISGVLV	431	
Db	366	YRRIIILGSGNNQELFVLDDTEFSFASLTNLNLPSTIYQRQT-----VDSLVDVPPQ	417	
Qy	432	VRNEDLRPLHY--NEIRNTESPGTGGRLAYMVSVHNRK--NNIYAVHE-----	478	
Db	418	DNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAPTFSHQHSRAEENNII PSSQITQIPLTK	477	
Qy	479	-----NGTMHLAPEDVTGFTISPIHAQVNNOTRTFISEKFGNQGDSLRPEQSNTRYAR	533	
Db	478	STNLGSGTSVVKGP--GFT-----GGDILR--RTSPGQIS	508	
Qy	534	TLRGN-----GNSNLYLRVSSLGNSIRVTINGRVYTSANVNTTNNQDVNDNGARFLD	588	
Db	509	TLRVNITAPLQSQRVRAIRVASTNLQFHTSIDGRPINQGNFASATMS--GSNLOGSGFR	567	
Qy	589	INMGNVASDNTNVPIDINY--TFNSGTQFOELNMIMFVPTNL	628	

Db 568 VGFTTFNFSNGSSVFTLSAHVFNSGNEWYIDRIEFVPAEV 608

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